

```

1 CGGTGCTGCC GGGCTCAGCC CCGTCTCCTC CTCCTGCTCC CTCGGCGGG
51 CGCGGGTGAC TGIGCACCGA CGTGGGGGCG GGGTGACCG CGCGTTCGCG
101 CGCGCGGCCA GCATGGCCAC CACCGCCACC TGACCCCGTT TCACCGACGA
151 CTACCAAGCTC TTGAGGAGC TTGGCAAGGG TGCTTTCTCT GTGGTCCGCA
201 GGTGTGTGAA GAAAACTCC ACGCAGGAGT ACGCAGCAA AATCATCAAT
251 ACCAAGAAAT TGTCTGCCC GATCACCAG AACTAGAAC GTGAGGCTCG
301 GATAATGTGA CTCTGAAAC ATCCAAACAT CGTGGGCTC CATGACAGTA
351 TTTCTGAAGA AGGGTTTCAC TACCTCGTGT TTGACCTTGT TACCGGCGGG
401 GAGCTGTTTG AAGACATGTG GGCACAGAG TACTACAGTG AAGCAGATGC
451 CAGCCACTGT ATACATCAGA TTCTGGAGAG TGTTAACCAC ATCCACCAGC
501 ATGACATCGT CCACAGGAC CTGAAGCCTG AGAACCTGCT GCTGGGAGT
551 AAATGCAAGG GTGGCGCGT CAGCTGGCT GATTTTGGCC TAGCCATCGA
601 AGTACAGGGA GAGCAGCAGG CTGTGTTTGG TTTTGTGGC ACCCCAGGTT
651 ACTTGTCCCT TGAGGCTGTG AGGAAAGATC CCTATGGAAA ACCGTGGGAT
701 ATCTGGGCTC GCGGGTTCAT CCTGTATATC CTCCTGGTGG GCTATCTCC
751 CTCTGTGGAT GAGGATCAGC ACAAGCTGTA TCAGCAGATC AAGGCTGGAG
801 CCTATGATTT CCCATCACA GAATGGGACA CGGTAACTCC TGAAGCCAAG
851 AACITGATCA ACCAGATGCT GACCATAAAC CCAGCAAAGC GCATCACCGC
901 TGACCAAGCT CTCAGCAACC CGTGGGTCTG TCAACGATCC ACGTGGCAT
951 CCATGATGTA TGTTCAGGAG ACTGTGAGT GTTGGGCAA GTTCAATGCC
1001 CGGAGAAAC TGAAGGGTGC CATCTCAGC ACCATGCTTG TCTCCAGGAA
1051 CTCTCTAGTT GGCAGGCAGA GCTCCGCCCC CGCTCGCTT GCGCGAGCG
1101 CGCGGGGCTT GCGGGGCAA GCTGCCAAA GCTATGTAA CAAGAAGTGG
1151 GATGGCGGTG TCAAGAAAAG GAGTTCAGT TCCAGGTCG ACCTAATGGA
1201 GCCACAAACC ACTGTGGTAC ACAACGCTAC AGATGGGATC AAGGGCTCCA
1251 CAGAGAGCTG CAACACCACC ACAGAGATG AGGACCTCAA AGCTGCCCCG
1301 CTCCGACTG GGAATGGCAG CTCGGTGCCT GAAGGACGGA GCTCCGCGGA
1351 CAGAACAGCC CCTCTGCAG GCATGCAGCC CCAGCCTTCT CTCGTCTCT
1401 CAGCCATGCG AAAACAGGAG ATCATTAAGA TTACAGAACA GCTGATGAA
1451 GOCATCAACA ATGGGGACTT TGAGGCTTAC ACGAAGATTT GTGATCCAGG
1501 CCTCACTTCC TTTGAGCCTG AGGCGCTTGG TAACTCTGTG GAGGGGATGG
1551 ATTTCCATAA GTTTTACTTT GAGATCTCC TGTCAGAA CAGCAAGCCT
1601 ATCCATACCA CCATCCTAAA CCCACAGTC CAGTGATTG GGGAGGACCC
1651 AGCGTGATC GCTTACATCC GCTCACCCTA GTACATGAC GGGCAGGTC
1701 GGCCTGCGAC CAGCCAGTCA GAGAGACCC GGGTCTGGCA CGTCCGGAT
1751 GCGAAGTGGC TCAATGTCCA CTATCACTGC TCAGGGGCCC CTGCGGCACC
1801 GCTGCAGTGA GCTCAGCCAC AGGGGCTTTA GGAGATTOCA GCGGAGGTC
1851 CAACCTTCGC AGCCAGTGGC TCTGGAGGCG CTGAGTGACA GCGCAGTCC
1901 TGTTTGTTTG AGGTTTAAAA CATTTCAATT AAAAAAGCG CAGCAGCCAA
1951 TGCACGCCCC TGCAATGCAG CCTCCCGCCC GCGCTTGTG TCTGTCTCTG
2001 CTGTACCGAG GTGTTTTTTA CATTTAAGAA AAAAAAAAAA AAAAAAAAAA
2051 AAAAAAAAAA A (SEQ ID NO:1)

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FEATURES:

5'UTR: 1-112
Start Codon: 113
Stop Codon: 1808
3'UTR: 1811

Homologous proteins:

Top 10 BLAST Hits

	Score	E
CRA 88000001156376 /altid=gi 7434378 /def=pir JC5636 Ca2+/calm...	1083	0.0
CRA 18000004937293 /altid=gi 125289 /def=sp P11730 KCCG RAT CAL...	1066	0.0
CRA 18000005054755 /altid=gi 1657464 /def=gb AAC48714.1 (U7297...	1038	0.0
CRA 105000014644765 /altid=gi 10443740 /def=gb AAG17558.1 AF233...	994	0.0
CRA 105000014644764 /altid=gi 10443738 /def=gb AAG17557.1 AF233...	989	0.0
CRA 18000004903800 /altid=gi 422770 /def=pir A46619 Ca2+/calmo...	986	0.0
CRA 18000005152785 /altid=gi 3241847 /def=dbj BAA28869.1 (D149...	986	0.0
CRA 18000004937876 /altid=gi 631810 /def=pir S43845 Ca2+/calmo...	985	0.0
CRA 18000004937877 /altid=gi 560653 /def=gb AAB30671.1 (S71571...	984	0.0
CRA 105000014644762 /altid=gi 10443734 /def=gb AAG17555.1 AF233...	976	0.0

FIGURE 1A

BLAST dbEST Hits:

	Score	E
gi 12893350 /dataset=dbest /taxon=960...	1778	0.0
gi 12790010 /dataset=dbest /taxon=960...	1463	0.0
gi 10142161 /dataset=dbest /taxon=96...	1443	0.0
gi 10158540 /dataset=dbest /taxon=96...	1366	0.0
gi 12796371 /dataset=dbest /taxon=960...	1356	0.0
gi 12340179 /dataset=dbest /taxon=96...	1320	0.0
gi 9342125 /dataset=dbest /taxon=960...	1185	0.0
gi 12386814 /dataset=dbest /taxon=96...	1180	0.0
gi 12421686 /dataset=dbest /taxon=96...	1172	0.0
gi 12886387 /dataset=dbest /taxon=960...	1063	0.0

EXPRESSION INFORMATION FOR MODULATORY USE:

library source (from BLAST dbEST hits):

gi|12893350 Placenta
gi|12790010 breast
gi|10142161 Skin melanotic melanoma
gi|10158540 Ovary adenocarcinoma cell line
gi|12796371 breast
gi|12340179 Uterus leiomyosarcoma
gi|9342125 Lymph Burkitt's lymphoma
gi|12386814 Small Intestine duodenal adenocarcinoma
gi|12421686 Breast mammary adenocarcinoma
gi|12886387 placenta

Tissue Expression:

Human fetal whole brain

FIGURE 1B

1 MATTATCIRF TDDYQLFEEL GKGFVSVRR CVKKTSTQEY AAKTINTKKL
51 SARDHQKLER EARTCRLLKH ENIVRLHDSI SEEGFHYLVF DLVIGGELFE
101 DIVAREYYSE ADASHCIHQI LESVNHQH DIVHRDLKPE NLLASKCKG
151 AAVKLADFGI AIEVQGEQQA WFGFAGITPGY LSPEVLRKDP YGKPVDIWAC
201 GVILYILLVG YPPFWDEDQH KLYQKIKAGA YDFPSPEWDT VTPEAKNLIN
251 QMLTINPAKR ITADQALKHP WVCQRSTVAS MMHQETVEC LRKENARRKL
301 KGAILITMLV SRNFSVGRQS SAPASPAASA AGLAGQAAS LINKKSDGGV
351 KKRKSSSVH IMEPQITVVH NATDGIKGST ESCNTTTEDE DLKAAPLRIG
401 NGSSVPEGRS SRDRTAPSAG MQPQPSLCSS AMRKQEIHKI TEQLIEAINN
451 GDFEAYTKIC DPLITSFEPE ALGNLVEGMD FHKFYFENLL SKNSKPIHIT
501 ILNHHVHVIG EDAACIAYIR LITQYIDGQGR PRISQSEETR VWHRRDGKWL
551 NVHYHCSGAP AAPLQ (SEQ ID NO:2)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

Number of matches: 4

- 1 313-316 NFSV
- 2 371-374 NATD
- 3 384-387 NITT
- 4 401-404 NGSS

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 5

- 1 33-36 KKTS
- 2 48-51 KKLS
- 3 259-262 KRIT
- 4 352-355 KRKS
- 5 353-356 RKSS

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 3

- 1 47-49 TKK
- 2 51-53 SAR
- 3 410-412 SSR

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 12

- 1 36-39 SIQE
- 2 51-54 SARD
- 3 79-82 SISE
- 4 94-97 TGGE
- 5 109-112 SEAD
- 6 385-388 TTTE
- 7 386-389 TIED
- 8 387-390 TEDE
- 9 404-407 SVPE
- 10 410-413 SSRD
- 11 465-468 TSFE
- 12 534-537 SQSE

[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

FIGURE 2A

Number of matches: 4

- 1 302-307 GAILIT
- 2 375-380 GIKGST
- 3 378-383 GSTESC
- 4 400-405 GNGSSV

[6] PDOC00100 PS00107 PROTEIN_KINASE_ATP
Protein kinases ATP-binding region signature

20-43 LGKGAFSVWRRVCVKISTIQEYAAK

[7] PDOC00100 PS00108 PROTEIN_KINASE_ST
Serine/Threonine protein kinases active-site signature

132-144 IVHRDLKPENLLL

[8] PDOC00364 PS00402 BPD_TRANSP_INN_MEMBR
Binding-protein-dependent transport systems inner membrane comp. sign

405-433 VPEGRSSRDRTAPSAGMOPQPSLCSSAMR

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	195	215	1.665	Certain
2	319	339	0.818	Putative

FIGURE 2B

BLAST Alignment to Top Hit:

```
>CRA|88000001156376 /altid-gi|7434378 /def-pir||JCS636
      Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123)
      II gamma-E - human /org=human /taxon=9606 /dataset=nraa
      /length=556
      Length = 556

Score = 1083 bits (2771), Expect = 0.0
Identities = 534/577 (92%), Positives = 539/577 (92%), Gaps = 12/577 (2%)
Frame = +2

Query: 113  MATTATCIRFTDDYQLFEELGKGAFSVVRRVCVKKTSTQEYAAKIINTKKLSARDHOKLER 292
           MATTATCIRFTDDYQLFEELGKGAFSVVRRVCVKKTSTQEYAAKIINTKKLSARDHOKLER
Sbjct: 1    MATTATCIRFTDDYQLFEELGKGAFSVVRRVCVKKTSTQEYAAKIINTKKLSARDHOKLER 60

Query: 293  EARIORLLKHPNTVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSEADASHCTHQI 472
           EARIORLLKHPNTVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSEADASHCTHQI
Sbjct: 61   EARIORLLKHPNTVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSEADASHCTHQI 120

Query: 473  LESVNHIIHQHDIVHRDLKPENLLASKCKGAAVKLADFGLAIEVQGEQQAWFGFAGTIPGY 652
           LESVNHIIHQHDIVHRDLKPENLLASKCKGAAVKLADFGLAIEVQGEQQAWFGFAGTIPGY
Sbjct: 121  LESVNHIIHQHDIVHRDLKPENLLASKCKGAAVKLADFGLAIEVQGEQQAWFGFAGTIPGY 180

Query: 653  LSPEVLRKDPYCKPVDIWAQGVILYILLVGYPFPWDEDQHKLYQQIKAGAYDFPSPENDT 832
           LSPEVLRKDPYCKPVDIWAQGVILYILLVGYPFPWDEDQHKLYQQIKAGAYDFPSPENDT
Sbjct: 181  LSPEVLRKDPYCKPVDIWAQGVILYILLVGYPFPWDEDQHKLYQQIKAGAYDFPSPENDT 240

Query: 833  VITEAKNLINQMLTINPAKRITADQALKHPWVQQRSTVASMMHROETVECLRKFNARRKL 1012
           VITEAKNLINQMLTINPAKRITADQALKHPWVQQRSTVASMMHROETVECLRKFNARRKL
Sbjct: 241  VITEAKNLINQMLTINPAKRITADQALKHPWVQQRSTVASMMHROETVECLRKFNARRKL 300

Query: 1013 KGAILTIMLVSRNFSVGRSSAPASPAASAAGLAGQAAKSLINKKSDGGVKRKSSSSVH 1192
           KGAILTIMLVSRNFS                                AAKSLINKKSDGGVK + ++ +
Sbjct: 301  KGAILTIMLVSRNFS-----AAKSLINKKSDGGVKPQSNKNKSL 339

Query: 1193 L-----MEPQITVVHNAIDGKIGSTESQNTTTEDEDLKAAPLRITGNGSSVPEG 1336
           +                      MEPQITVVHNAIDGKIGSTESQNTTTEDEDLKAAPLRITGNGSSVPEG
Sbjct: 340  VSPAQEPAPLQTAMEFQITVVHNAIDGKIGSTESQNTTTEDEDLKAAPLRITGNGSSVPEG 399

Query: 1337 RSSRDRTAPSAGMQPQPSLSSAMRKQEI IKITEQLIEATNNGDFEAYTKICDPGLTSFE 1516
           RSSRDRTAPSAGMQPQPSLSSAMRKQEI IKITEQLIEATNNGDFEAYTKICDPGLTSFE
Sbjct: 400  RSSRDRTAPSAGMQPQPSLSSAMRKQEI IKITEQLIEATNNGDFEAYTKICDPGLTSFE 459

Query: 1517 PEALGNLVEGMDFHKIFYFENLLSKNSKPIHTTILNPHVHVIGEDAACTAYIRLTQYIDGQ 1696
           PEALGNLVEGMDFHKIFYFENLLSKNSKPIHTTILNPHVHVIGEDAACTAYIRLTQYIDGQ
Sbjct: 460  PEALGNLVEGMDFHKIFYFENLLSKNSKPIHTTILNPHVHVIGEDAACTAYIRLTQYIDGQ 519

Query: 1697 GRPRISQSEETRWWHRRDGKWLNVHYHCSGAPAAPLQ 1807
           GRPRISQSEETRWWHRRDGKWLNVHYHCSGAPAAPLQ
Sbjct: 520  GRPRISQSEETRWWHRRDGKWLNVHYHCSGAPAAPLQ 556 (SEQ ID NO:4)
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FIGURE 2C

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF00069	Eukaryotic protein kinase domain	309.5	4.1e-89	1
CE00022	CE00022 MAGUK_subfamily_d	295.5	3.9e-87	1
CE00359	E00359 bone morphogenetic protein_receptor	14.8	0.0017	1
PF00534	Glycosyl transferases group 1	3.3	9.1	1
CE00031	CE00031 VEGFR	0.3	3.2	1
CE00292	CE00292 PTK_membrane_span	-59.7	1.5e-05	1
CE00287	CE00287 PTK_Eph_orphan_receptor	-63.5	0.00035	1
CE00291	CE00291 PTK_fgf_receptor	-90.9	0.0016	1
CE00286	E00286 PTK_EGF_receptor	-131.8	0.0056	1
CE00290	CE00290 PTK_Trk_family	-154.9	0.00012	1
CE00016	CE00016 GSK_glycogen_synthase_kinase	-180.4	1.2e-06	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00534	1/1	31	65 ..	161	195 .]	3.3	9.1
CE00031	1/1	133	161 ..	1068	1093 ..	0.3	3.2
CE00359	1/1	132	186 ..	272	327 ..	14.8	0.0017
CE00286	1/1	14	252 ..	1	263 []	-131.8	0.0056
CE00290	1/1	15	253 ...	1	282 []	-154.9	0.00012
CE00291	1/1	14	267 ..	1	285 []	-90.9	0.0016
CE00292	1/1	14	267 ..	1	288 []	-59.7	1.5e-05
CE00287	1/1	14	270 ..	1	260 []	-63.5	0.00035
PF00069	1/1	14	272 ..	1	278 []	309.5	4.1e-89
CE00022	1/1	10	305 ..	13	316 ..	295.5	3.9e-87
CE00016	1/1	1	345 [.	1	433 []	-180.4	1.2e-06

FIGURE 2D

1 TTGCCCCGCG CCTGGTCTCC CTGATCAACC CGCGCCTGAA GGGTTTCTTT
51 CTAATAATGG CCTGGTGTCT TGCGCAAGTC TAGACTGTCA GCTCCAGAG
101 GGAAGGCGGC TGGCAGCTGG CTCTGCGCAG GCTGGGGGCG CTTCCCGGGC
151 GTGCAGCCTG GCACAGGCTC CTTGACCTTG GCTCTCTCCC CACGTGCTAG
201 GAGCCCCGTT GGGGGCTCGG GACCCGCGTG TAGGACCCGT CCAGAGAGGT
251 CAGTGGTCCA GACTCCTACA CTCTTAACAC ATGCAACCTC GCATGCACGT
301 TCCCGAGCCC GCGCGGGGTC CGCCCCGGGA CAAGCCATA AGTCGCGAAC
351 CTTCAGNNN NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN
401 NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN
451 NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN
501 NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN
551 NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN
601 NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN
651 NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN
701 NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN
751 NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN
801 NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN
851 NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN
901 NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN NNNNNNNN
951 TCGACATTAA ATTCAAAAT GTTTCCTCC GTTGTGACT TGTGGTTTAA
1001 CTATGTTCAA TGGTCTCAC CAAGCAATTT TGCAAAATAG TTAACTTATT
1051 CTCTTTTCTT TACATGACTT CTTGACTTTG AGCATAGTT AGGAAAGGTT
1101 TGCTCCTCT CACATAGAG TAAATTTAT CCACATTTTC ATCTAGGATT
1151 AGTGCTCATT TTTTATTAT TATGAATATC TTCTTCATTT GGGGTTTGT
1201 CATGTATATT CCATGAACAA TGGACGGGG TGCGAGCATTT TAGCATCAGC
1251 TATCCCTTC CCATCCGCAA TGAGCTGGCC GCTGCAGCAG CCCCAGCCCC
1301 CCACCCCTAC CCGGGGGCC GAGCCCGCC ACTGCAGCC CCGCCCGCC
1351 CGCCCCCA GAGGTTTCA GAGCTCAGAG TCGAGCTCC GGTTTGACCG
1401 GAGGTTCAAG GAAATAGCA TGGGAAGGG AGTTCCTGAT GTCTGACTGT
1451 GTCTCTCTT CCTTGTCTGT CAGTTGAGCC GGGATGCAGT GAGATGAAAC
1501 CGGCTGTGG GGGGTTTGG CCTCACTTTG CCCATGGTT GAGGAGATT
1551 TCTCTTTTCA GGGATGATAC CCTCTTTTAA ATCTTTCTTT CCCCAGCTTT
1601 CAGCTGTTC TGCTGAGAGA AGGGCAGGT CTCTCTGCTC CTTTCTGCCC
1651 TGGTCTCTT GCGCGGACC GCAGGGCTGT CTGAGATGCA GCAGGTGTGT
1701 GTTTTCAGCA TCGCCACCC GCTCTGATG TCGAGCTGGA GGTGGAGGCT
1751 GTTGCCCTGC CCAGGACTG GATGAGGGG TGGGAGCGCG GCAGCCACC
1801 CACATCTGT CAGTGCTCT GGTGGCCGC GTCTTTTGC CTCTGTGTG
1851 ATGGTGGTG TCACAGCGCC GGTGTGTGT CATGTAGTG AGTGTGCTA
1901 GAGGTCTGT GGTGGGAGCA TCATGTGCC CAGACTTCAA GTGTGTCTGT
1951 GTCTCTCTC CTGCTCCGT GTCCAGTTC TTTTCCCTTT CTCCCTCCAG
2001 GGGTGTCTT CTGTGGTCC GCAGGTGTGT GAAGAAACC TCCAGCGAGG
2051 AGTACGAGC AAAAATCAT AATACCAAG AATGTCTGC CCGGGGTGAG
2101 TGTCCCTGT CTGACCTCT TCTGAGGGT GCTCCAGGG GCATGGTTT
2151 CTTTGTAGGA AGCCCCAGGA ATTGGGGGT GTGGTTTAA GCCTTGGAG
2201 AGGAGTTGA ATTTAGACT GGTGGACTT TGTGTAGGC TGAAGGCAGA
2251 AAAGGAGTT CATGGGGAC TGAAGCGCC CAGGTACAA AGAATGAAGG
2301 AAGAGATGA AGTAGCTGA GTGGCCCCA AAGGCTCAAG GGAGTTCCGT
2351 CTTCAGGGAG GTGAGGATA TGGGGTAGT GGGTGTACA GAATGGGAG
2401 CTCTTAATT GGGCATTTG GAGCTCTCC CTTTGGGCA GTGGTGGCTA
2451 CTGAGGCTT TCTGTGTTT CTTCTTACC ACCGGCTGAG TTAGGATGGA
2501 AATGCAGTAA GTGAGCAGT CTGACAAAG CAGCTCCCC TGCCACCAG
2551 GCGGAGAAC AGACTCCAA GGAAGGGA TCTGTAAACA TCAGGGGAGG
2601 CTGCTACTGG CGAGGGCTTC TCAGGAACA ATTCTGCCAG ATGAACTTGA
2651 TTGCTTTTGT GATCAAATTA CAAAGTTGTT GTGCGAGCAG CAGATGTAGT
2701 CTGTCCCTGG TGGAGGGTGA TGCTCATGG TCTAGAAATC CCAAGGCCCC
2751 GGTGTGGGCA GGAACGTGAC TGCTCCGAA CTGCACTGCC TCCGAGTCTG
2801 AGGAGCATAA AGGCCAAGG CTTGGGGCT CACTTGCGAG ATCTCCCAA
2851 GTACCTGAG CTGTGAGGT CAGGCGCTGT CTTTCAACC TTGAACCTAC
2901 ACTCTCTGAA CTCTCTATT GGTACTTGC AAACCTACCT CATCTGATAG
2951 GTGTAGACC AGCAATGTGT GAAGTGCTCT GGAACAGGT CTGGTGAATA
3001 CAGAGTTCAG ATCTCGAGG GCTGAGGGT GCAGCTGGG GACAAAGGTT

FIGURE 3A

3051 GTGAAACTCA GAGAAAGGAA TTAGGGCTGG GCAGTAGGAT GGCATAAATA
3101 TATTGTGAGC CAGGACACAT GOCCTGGGGA AGACATGGGC TTTCGGCCAAT
3151 AATGACACGG GTTCTCTCTG GATAAGAGAC ATAATAGATG TCCCAAATGC
3201 TTAGAGAAGC TCTACAATTC CACGGGCTTC TGTGTGTTTG GCAGTTGTTT
3251 TGGGACCTGT TTAGCAGGGC CGTGTCCTCT CCTGACTTGG GGACTCTCTC
3301 TCCATCCTCT TGGTAGGGCA CTAATTCCTG ACTCCCATCC AGCTCCATCT
3351 CTGTCTGTTT GGTACATTG CCTATAAGT TGGACTTGTT TGTTTTCTTT
3401 CTCCTGGGT ACCCTGAGTC TGAGGATGGT TGCCATAGAG ATATGTGGGC
3451 AGTCAGATAC CCTGGAGTGG GGGTGGGGGG GACAACAGGG GCTGGGCTCT
3501 CTGGCAGACA TCCTCTGGCC AAGGATGGAA GGTGCAGGCA GGAACAATGG
3551 CTTGAGGCTG GATACCTCTC TTGCCCACAC AGCAGAGGCC TGGTGCAATC
3601 GAAACAGGGC TGGCATCTGG TGCTCCAGT TGATGATGCA ATGCTTTGCT
3651 CTCCTCATCT CACCACTGTC CTCGACCCA TGGGTAGAG AAGGAGAGAT
3701 GGCCTGGAGC CGAATTCCTG GATGTGAGGA TAGGTGATGT GGTGACTTCC
3751 TGCAGCTGCC TGACTGGGGC TTTCATTTCC TACTCCCTCC CTACCTGCGT
3801 AAATTTCCAT GACCTGTTG ATAGCTCCCT TTTCCTTCC TCACCTCCTT
3851 TTAACTTGT CCACTCTTTC CCAATGGATA TCTTTCCCTG GCAAACCTGG
3901 ATGAGACTTG ATTCTCGTT GATTTTTTTT TTTTCCCTCT CAAGAAGAGG
3951 ATTCTTGTGT AAAAGTATAT GCTTCAGACA GCACTCCCTC CTCCTCCAG
4001 ATGATATGCG CAAGACTGGG CTCCTGTGTG TGGCTCATG TGCCAGGTG
4051 ACTTTGGGAC AGAGGCACAG ATGATAGGCA CAGATGCCAG CCAGAGGGGT
4101 CAGAATGTGT AAGTCCAGC CAGTACTGTG TGGAGGTGG AAAGTGGAAA
4151 GGGCTGTCTT TGAGATGGA GGAACAAGG TGGGGCTGGA CTATAGGTGT
4201 GGGCATGGGA GATGTGAAT CCTGGAGACA TCTGGCCAG GGTAGCCATG
4251 GGCCTGTTCC CATGGGTTA GGGAGTGGG GCACTGGCTT CCTGCGAGC
4301 TCTCAGTTTA CACTATATAT TTTATAAAGG TGCCGCCACT GGAGCTGGGT
4351 TTCACATATC GCTGTCCTCC TAGGTCTCCG CAGGTGTGG ATTTCTGTGT
4401 CTGGGAATGT CGTGGGCCCA CCAGGTCTAT CTGTGAAGGT CTGAAGGGGC
4451 TTGCTGTGTT CACTGGGTCT TCCCTGCTCC TGCTTTCTTT GTTTGTGATT
4501 CTCCTGGCTA CAAACTGAAA AGATAAAAAG AGGGTATAGA GCTGTTCTCT
4551 CTTCGCATCC CTGGTGAGGT GGCCTAGGAT CAGGAGAGG GATCACCCTG
4601 TCTCTCTGGG GGGTCCAAAT GACACAGGAA GCTCTCTTTT GGGCTGTGT
4651 GTCCTGTGAC TGTGGCTCA GAGGCCACA TGGGGGCTA GGTGCAAGG
4701 TGGGAGTTC ATGCCGATAT GCGTTGAGCA CTGTCTTTGT CTGGGGGCTT
4751 GTCTACATAA AGTCACITAA AGTCACATAA GGTCACTCCG TTTGCTTCAG
4801 AACGGTGATA GGAGTGGAGC TGGGCTCTTA AGGGAGCCCA TGGTTCCAG
4851 CTTAGCTCCA CTAGGCCGAA GGAGGCATTT AAAATAGGCT TGGATGCAGG
4901 AGCTAGTGGG CCAGGTGATG GCAATGATAA GTCTGTTATTT TAAGATTTAA
4951 GAGCAACCCC CTCAGGAGC CTGAGCCCTT ATGCTTTTTT TTATTTTAA
5001 ATCTTCATAT TCCCTCTCTA TCTTTATTTA TATGCATACA GATTTTCACC
5051 TCGTGGAGCA TAACATTTTA TATCCCTGCT TCTTTGCTTA TATCCAAAGC
5101 ATTTCCCCCA TATTACTACA GTTGAAGGGC AAATGGTCTT TCTCTTACG
5151 TGTGTTAGGA TTTATCCCTA AAACAATCAG CATCACAAGA AACTTCTGTA
5201 TATGTAACAT TTATCTGGAT TCCAGTTGCT TTTACCAAGA TAGATACCTG
5251 GGTAATGCC TTTGGCTTAC TAAGAGATGC TACCGGAAC AGTGTTTTGA
5301 AATCTGTAT AATACITTA CAATTTTAT TAATCTGTAC ATTCCGTGTG
5351 AAGAAATTTT TTTTGAAGCT AAATGTAGC AAAAGCTTTC CTCCTTGIGA
5401 GGACCTGAGA GGTGAGGGAA GGTCTCTTAT GGTCTCTAT ACTCTGCTAT
5451 GGGCAGGCC TAGCGAAGTG CCTGACGTAT GGCAGCCACA TACACATTAA
5501 ATGAATGGGT CAAGAGGACT ATGTAACCAA TCATGTTGTC CTTTGGCTT
5551 TGGCTCTAG GAAACTCAGA GTCAAGTTGC CAGAGCCCTT GTACCTGCT
5601 ACAGACTTGG GTCTCTCTT TCTGATCCAG GGAGCCAGC TGCAGACTG
5651 ATACGGCTGC TGAAGAGAG GACAGATGAG GATAAAGACC TGTCTTGGG
5701 GCATAAGGCA GAGTGGGAGA TGTAGGCAGA CATTTAGCTG ATGATTCTCT
5751 CTCTCTGTC ACTAAATGGC ACTATAGGCG CACTGTGGG ATCTCTTCCA
5801 GGTAGTCAAT TTCAATTTTA GTGTGGTAA GATCACCTT GAGTACTAGT
5851 TTAATAAATA CAGACTTCTG GGTCTTAGCC ACAGAGATTC TGTCTTAGGA
5901 GGTCTAGGCT GGAGCTGCAG AATCTGCATT TTTAACACAT GCTCCAGTGA
5951 ATTTCAATGA GGTGAGGCAT GAGCCACTCT TTAAGAGATG CCACTAATAA
6001 TCTGCAACAA CAGTTGCTCT TGCCATGCC TCTGGAATTC AACAGACACA
6051 CCTTGGGCCA TCCTTCTCCA GATTGTGTGT CTGCCACTAT GTGGCCATCT

FIGURE 3B

6101 GTGCACATGG GCTGTTCTGT GATTAGGGGC CTGTTCTGG GCGTGGGAT
 6151 TGGGGTGTCT GTGTCAGG CTGGGCAAG CTGGGTGGCT CGGGTGTGG
 6201 CATGTTGGCC ACCAGAAGG TAAAGGCTGT CCCTTCTGG GTCCAGCTGG
 6251 CCGTGGGGAC TGAATGGGA TCCCTGGAT GGTGCGAGCT GAGAGTCCC
 6301 GCGCCCTTAG TGTGGGCTG AGTAGCCCC ATGACATTG TGTCCCCTGT
 6351 GGTATCTCCA AGTAGACTT TCTGTTAAG GATCTGGGTG AAGTAGGGGA
 6401 AAGAGAAGGG AGGGGAAGC AGTAATGCAG GGAGTGGAG AAGGAAGAGA
 6451 AATOCACACA GCACTGGAAC ACAGGCTCG AGGAAGCAT TAAGGAGCT
 6501 GTGTGGGAAA CCAATGCTTC CTCTGAGGA TAAACAGGC CAATTCTGT
 6551 AAACAGAGAA ATGGGCATCC TGCAATCAG TGATGGAGG CCCTACTTT
 6601 CTCCTCTGAA GGGATGGAAG CCGACTGCAG GTCCCTCTGT GCAAAGGCTT
 6651 CTGCCAGGG GCTTTTGTCA CGCGGTACG TTGAGCTGTG GCGCTTAGCA
 6701 CACACAACAC TGGCCGTCC CCGTCCCTC CCACCTGTCT TCTAGAGTG
 6751 ACTTGGGGT CTGCACTAG GTGTGGGAT GGAGGTGGGA AGGTTGCCCT
 6801 GTCTGTCTAG GGAGGCCCC GCTTCTTCC TGCTGTCTC TCTGGTCCC
 6851 TGTACCCATA CCGTGTCTG AAGCTGTGT GAAACCTAG AGGTGAGTGG
 6901 CTGACCCAT TCTTGTCTA GACTGGAGT AGGAAGGGG AGGCTGGGTG
 6951 TGACCATTC TGCTCCATC TGTATGCTG CTGCTCTCTG AACAGCTTG
 7001 GCAGACCAAC AAGGCGCTGA TCCATGGGT GCGAAAAGG TGGTACAGG
 7051 AGGAGATGG CACTTTGCAC CTCCTGAATG CCCTCTCTGA GAGCCCCCTT
 7101 GTACCTTACC CATGGCAGA CAGATCTGC GCGAGACCG TGGGGAATC
 7151 AAAGCAGAAA AGCTTTGTCT GGGGTCTTT TTTTCTTTT TGGTTTGTG
 7201 CTGAGGTGC CATGACTTT GCGAGGCTC AGACCCAGG TCCTCAGGCC
 7251 GTGTGGGCTC CCGCCTCTC TTGGGCGCTT TCTTAAAC ACAGGTCTG
 7301 GATACTTTGT TCTGTGATG AATCTTGGCA TATCACTCA CACTCTCCA
 7351 TCTAGGCCC AAGCTCCAG CCGTGGGAG CAAATCCCTC CTGTGTCTG
 7401 GCTGAGGCG CATTCGGTC TGTACCCAC TCTCTGGCT GTGGGGTGG
 7451 GAGATTCCA GCGCTCTC CCGAACACA TCTCGCTTC CTGGGCGCTA
 7501 TCAGCAGAG CCGCAGCTC CATCTGCTC CCGCTTTTC TCTCCCTTT
 7551 CTTTCCCTC CCGCTGCTT GCTGCTGCT TGGAGGAGC TATTTTAGG
 7601 GCGTGTCTC TGGGATGTT TACTTGGGC TGGTTACAT GAAGGAATG
 7651 TCACCAAAAC AGTGGGCAA GCGTGCAGC ACCGGAGCC CTGCGGGGG
 7701 GCATGGAGAA CAGACGCTG ACGCTTTCT GCGCCCTGAG AGCAGCCAGA
 7751 GTGCCCCAG GCAGAGCTT GCGTCTTGG GCGTGTCTG TGACCCCTG
 7801 GGGATTTCT CTGTCAAAG TCAATGAGG CCGTTTCTG ATAGGGCAT
 7851 TCTTGGAGC TCTGCTTCC CTGCTCTGA GATCCAGAG CCAAGTGGG
 7901 GCTCAGGCT TGTGTGACC AAGTTAAAC TCGTTGAGT AGGGTTGAAG
 7951 ATAAGGGGAG GATGCTGGT ACATGCACAG AGCCTTGGG GTTACATGG
 8001 GACATTTCA GCGCCGCTC CTCGTATCA CAGCCCCAG CTAGTACCA
 8051 GGTGTACAT GTGTAGGGA TTAGAAACA TGGTCTGCT CTGTGTGTC
 8101 GGTAGGACT TGTCTTAAAT TGGGACTCT TTGCATCTT AGAGTGAAT
 8151 TCAAGAGGA AGGATGTGG CATCACAGT TCAGGGTGA GTGGGTGGGA
 8201 TGTGGCTTG GATTCCTAC TGGTCTGCT CCGAGGCCA GGGCTGTGA
 8251 TAAGCAGCT GGAAGGTGG ATTATGACAT CAAATCCCTG CGATGTCTT
 8301 GTTCTGTCT CTCAGAGTC CAAGGGGACC AGAGGGGCG CTCGTGTCT
 8351 TGGGAAGAG ATCAAAGGA CTCAGGAGG CAGCAAGTA GCGGCTCTC
 8401 CATGGAGCC TGAATCAGT GGGGTGCGAG GAAGTTCTC ACATCCATG
 8451 TTAGGGTAT AGGCACAGC CTGCAAAATA CCGTTTGCA AGTTAAGAT
 8501 GTCTTTGAG TTGGAACCTG GGAGAGTCT CAGTCAGAT AGGAATGTG
 8551 ATCTTTTCC ACCTACAGAG GATTGTATG TTACGTGGCA GCAGGATCT
 8601 ATTTGAAGCT AGTGTGGCA TTTGTGTTT TTTTGTAGGA AATGTACT
 8651 AAGTCAAGCA GCGCCATCC TGAGAGGGC ATGGAGAATC TGTGGCAGC
 8701 CCGCTTGGC CCGCTGACT GCGAGAGGA GGAAGGGCA TTGGAGTAGG
 8751 CTTCTGTCT CAGGCGAGG GGGGAGGTG TTGAGGGCA GCGTTGTG
 8801 ACCCTTGGC TGCAAGCTAT CAGTCCCTA TCTGCTTCT CTTTCTGCT
 8851 TCGCTTGGT CATCTGGTA CTTCTGTCT CCGTCTCTG GAAATCTGG
 8901 CAGCTTGGC CAGTCTGA AGCCTTGGG CAGAGGGCG GAGAGGTGG
 8951 GTTCTTAGGA TCTTGTCTC CAGGGGCTG GCTCTGGCT GGGCTCAGC
 9001 CACTCTGCT TAGGCAGGCT GCTGGGAAA GCGTGGAGCT GCTTCTGCT
 9051 TCTGCTCTG TTGCCCTC TGCTAATGAT GGGGAAAAC TGCGAGGGC
 9101 TGTGTGTGA GCTGGCTGA AGGCGGCG GGTGGGTCT CCGATGGCA

FIGURE 3C

9151 GTAGCACACA GGCAGGCAGG AAGTGGCCCT GTGCAAAAGC GGAAGTGGC
9201 AGTTGTCAAA CAGGAAGGGG GGGCTGGGC TGTGGTAGGG GCGGGATGA
9251 GCGTGGTAGA AAGGTGCGTG GAGGAGGGTC CACCTTGGAA GGTCGTAGCC
9301 TCCTCCCTAGT GGTACTGGA AGGAGGGGTG TCTCAAGGGG AGACACCTTT
9351 GCAGCACTTT GAGATGCGA GGCAGGGCCC TCCACTGTG GACCAAGCCC
9401 ATTACATGGC CTCGCCCTTT TTGGGGTTGG AGATGCTGGG TCCAGCTGGG
9451 ATGCCCTTGC TTTTGGGAAA GATGCTCTAG AAACCACTAC TCCATCCTGG
9501 AAGCCCTCTG CCGCCACTGC TGCTGGGATG GAACCTCTGC TTTTGTCCAG
9551 CCGTGGGCCA GCGCTGGATG TGACTACAGG ACAGGAAGTG TCAGGGGAAG
9601 AGACAGGAGA CAACAGCTGG AGAGGCTGGG TGGTGGCCGG GCAGTATGTG
9651 GCAGCAGGAA CCGGAGAGC GGGCAGGTA GAACTGCTC TGTTCATTGA
9701 GGAGAGCTTG TGGATGGCAG GGTGCCACGG CTGCGAGGAA GAGGAGGGAA
9751 GCGACAGTG GCACCTTCTG CGCGTTCCCT CTCCTCTGTA GGAGCCCTG
9801 TTGCTGCCCA TCACCTGCAG ACTGTAGACA CAGGTGGGCC CCGCAAAAC
9851 AGGGAGGGAC ACTCCACCTC CAGGACTGCA ATGGAGGACC ATGTGGGGAG
9901 CCGAGAAGCC AGGCAGGAGG GCTTAGTTGC TGTGTGCGAG ACCCTGCATC
9951 TGCTGGGCT GAGGGGACAG TGGGTCCAT TCACAGTGTG TCTGGTGATA
10001 GCTGTGCCCA CAGGCCAGC CCAGGAGACC CTGTCAAGCT TCTCAGTGG
10051 CCGTGGAAA GGAGCTATAT GGCAGACCTT ATGCAAAACT CTGACCTGT
10101 ACCACTCTAG TTAAACCTCA GATCTGTCTG TCTCTATTTT AGAAGTGGG
10151 AACCTCTTGG CCGGGTGGG TGGCTCAGC CTGTAAATCC AGCACTTTGG
10201 GAGGCCGAGG CAGGAGGATC ATAAGGTGAG GAGATGAGA CCATCCTGGC
10251 TAACACAGTG AAACCCCTG TCTACTGAAA AATACAAAAA AATTAGCCGG
10301 GCATGGTGAT GGGCGCCCTG AGTCCAGCT ACTCGGGAGG CTGAGGCAGG
10351 AGAAGGGGT GAACCTGGGA GCGGAGCTT GCAGTGAGC GAGATCATGC
10401 CACTGCATC CAGCTGGGC AACAGAGTAA GACTCCATCT CAAAAAAG
10451 CAAAAAAGC AAACAAAAGA AGTGAGGAC CTCCTTCCCA AGATATGTG
10501 CCGGCTCAC TGTCTACCT ACTTTGGGTC CTAATCAAT GTACCTCCT
10551 TACTGAGGCT TCTTGGACT GCGCTACTCA AATCTGCACT CCGACTTTC
10601 TCTGCTTTT CTACGACGA CTTCGCGTGA CATCTAACGT GCTGTAGT
10651 TTTCTTACTG TCCATCCCTC CCGCATACAC AACCCTAG AGTGTAGCT
10701 CCATGAGGC AGGGATTTT GTCTGTGTG TTGCGCACTG TCTTCTAGC
10751 ATCTGAATA CTGTCTGTA CATAGTAGGC CTGAGTAAT ATTTCTTTT
10801 TTTTTTTGAC TTGCTCTGTC ACCCAAGCT GGAGTGTAGT GGGCAATCT
10851 TGGCTCAGT CAGCTCCAC CTCCTGGGTT CTAGTGAGCA CATTGGCTA
10901 AATTTTGTAT TTTTAGTGA GATGGGGTTT TGCCATGTG GCGAGGCTG
10951 TCTTGAACTC CTGACCTCAA GTGATCCACC CACCTTGGCC TCCAAAGTA
11001 CTGGACTGGG ATTACAGCG TGACCCACCG CGCCAGCCA CGATAAATAT
11051 TCTTGAAGG AATGAATGAA GCTGGGGTGG GTTAATAGC TTGCTGGATG
11101 TGGCAGTGT GGGCTCAATC CAGGCTGTG TGACTTCAA ACCGATGTGT
11151 TGTAAATTC CATATCCAC AGCTTAGAAT CAGAATGAGG ATCAAGGTAT
11201 AGTCTGGGG TTGAGAGAAG ACCTGGGCT TGCGGGAA ACAGGCTCA
11251 GCTCTTGA GTTAAGGCTG AACTAAGAGG CTAACAAGGA CCTCTGGAT
11301 GCTGGGACG TCCCTTGGG AGCTGGGAGC CTGAGTCTGT GTATCTCTC
11351 TCCACTCAA GTCACTGGTA AAGCAGAGTG CCGTTATTTT TAGTGTGT
11401 GCTGTGTGG GACTGTAAAC ATTAGCTAGT AAGAGACTTA AGGAAGGAGA
11451 TAAACATTA TCTTCTGGG CTTCCCTCAG CTGCCACCTC CGCATGTCAA
11501 GATGCTGTTC TCTTGCACT GCGCAGGCAA CCAAGCTGA GAGTATATGG
11551 CTGGAGGGTG GTAGGTTTG TGCCAGAGA GAGGGCGTG GGTCTGTAGC
11601 TTTGGGGCTG GCTGGCTTGG TAACCTCATC TCAAGTCCAG GATGGAAGG
11651 AAGGTGGGGT CATGTCAACA TCTGCCAGA TCTGGAAGAA GCAAGCCCC
11701 CAGCCACCAG GCAAGGCTGT TACAGCTTC TTGAGTGCCT CGCTCTGGA
11751 GGTACATGG CACATCCCTG TGCCGGGAC CAGGGATGC CAGGTGATCT
11801 GGGAGTTGG AGTTACTTGG GGTCTCTCTG GCTGCATCT GGTGGTGT
11851 CATCTGAAC CAGGCACAG GAAGGAAGGC CTGACCCAGA TCTTTGGGA
11901 GCTGGGACG ATTAGCTGG CAGCAGGAAC TAATCTCTGT CTGTCCCAAC
11951 CTCCTTCCAC AAAGTAGAGC TGTGTCTAGA GGGAAAGTTT AGGACAAAGC
12001 TGGTTTGGT TAGTGAACA ATAAATGTGA ATTTCTCTA GTCCATAATC
12051 CTTACATTA CTACACAGA CAGTCTGAG TTTGAATCCC CTTTATATC
12101 CTTTCTGCT GTGGATCTT GGGCAAGTGA CTTAACCTCC CTGGGCTCC
12151 GTTCTCTCA TCATCTGGA ATGTGGACAA TCATAGCAIT TACCTAATGG

FIGURE 3D

12201 GATCATTTGTG AGGGCTGTGG GAAGATTITAC AGAAGCTTTT TGCTGTTTAG
12251 GGTAGAGGCA GGGAGACAGG AATAGCTTGG CAGCTATGGA TGTGAAGGCC
12301 CCTGCCGGG CCTGGATAAT TCAGGGTGAA CTGGACTCTC TTCTTTTTCG
12351 ACCCCCTCCA AAGCCTAGAG TCTTAACCTA ACTCTACCA TTCTTTATCT
12401 GGCATATAA GCACAGGGGT GGAGAAAGAG GGCTCTAGGC TCAGACCAAC
12451 TGCATCACTG CCTGTTGGTG TTACCTTAGG CAGATTACTC TATCTTTTTA
12501 AACCTGTTTC CTGGTAATA TAATAGAGCT AATCAGATCC CTACTTCACA
12551 GAGTTTCTGT AGGTATGAAA TATGGTAATC CATGCCCTCG CCTGACATGT
12601 AGTCAGTGA TAGTAAGCGA TTGTTATGGC GACTACTGTT ATTAGTAAAC
12651 CCTTATTAAG CCGCTGTTTA CAGAAAGAAC TCTAGAAAGC ACTACCTGGA
12701 AAGGTACCCC CGCCTTGGAA GAGCTTGGCA CTGAAAGATA ACTGATGTAA
12751 TATATGATGT GAGAAATCGTG AGAAGTGCAAT TGGGAATCG GGGGGGGGGG
12801 GGTGGAGTAG GAGGGAGAAG TCACAGTCTA CCGAGAGGAG CAGGGAAGAC
12851 TTCATGAAGG AGGTGACTTT TGGCAGGATT TCAGCAAGTA GAAAGAGGGA
12901 AGCAGCTGG GGGAGGGCTG TGAGGCTCC GTGCTGTGAG TAGCATCTC
12951 TCTTCCACG TACTGGAGCT CTGCCCTCCT GTGGAAGGAA TTGACCCACG
13001 CAGCTCACTT GGATCTGGGG ACTTGTGGAT TTCTGGTTAT TCCACCAAAA
13051 CCAAGTAAAT CTGGAGTCTG AATTITGAAGA GGTCAAAGCT TACAGCCATG
13101 GTGGCCAGA GGACTCCGGG GAGAAGCAGG ATTTGTGTCC TGGTTTCTCT
13151 TTCTATAAAA TGGGCATCAT ACTAATGCCA CCTCCTAGAT TGTATGAGG
13201 ATAAATTAAG AGAGGAGCTT GCTGGGTGTA GAAGTAAGCT CTCAATAAAT
13251 GTTAGCTATT ATTATTTTAA GTCATCATTA TCTTGATCAT CAACCTCTTT
13301 ATTATCAGCA TCATTATGTT TCAGGCTTGC CATCAGGACT ATGTAGAGAA
13351 TATATGAAA ACCCTAGGC AGTGGCTAGT ATATATTAGG TGCTCAGTAT
13401 AACCTAGCTA TTATTAGTGT TCTAACAGG AAAGAGATTC TGGGCCAGGC
13451 GGGTGGCTC AGGCTATATA TCCAGCATTT TTGGGAGGCC GAGGCGGGTG
13501 GATCACCIGA GGTACGGAGT TCGAGACCAA CCTGGCCAACT GTGGTGAAC
13551 CCGTCTCTA CTAAAATATC AAAAATTAGC CAGGCGTGGT GGTGTGTGCC
13601 TGTAAATCCA GCTACTCGGG AGGCTGAGGC AGGAGAAITG CTTGAACCCA
13651 GGAGGCGAAG GTTGCAGTGA GCCTGATCA CACCACTGCA CCCAGGCTG
13701 GGCACAGAA CGAGACTCCG TCTCAGAAAG AAAAAAGAG ATTCTGGACA
13751 CCTGGAGCA CTGAAACCCCT GTTGTGGTGG AAAGAGCACC AGAGTTTATG
13801 TTGAATACCT GGAATCAAAAT CCGAGCTCTG CAGCTACCTG GCTGGAAGTG
13851 TGCAAAACCT CAAGTCAITTT CCTCATCTGG AAAAGGTTGT CATAACTATC
13901 TATCTGGCCC AGGCTGGTGG GCTGGTGGCT ATAGTTCCAG CTATTCAGGA
13951 GGCCTGAGTG GAGGATTTGC TTGAGCCGAG GAGTTTGAGG CTGGATCAT
14001 GCACTGACAC TCTTGGCTGA GGCACAAAGT GAGACCTAA AATGAAAGGA
14051 AAACAAGTTG TCTCCAGGAT TGCCATGACT TGCTGCATTA CTTACAGAGA
14101 TCATACAAA TGCAATAGTA GTACCTGAAC TGAAGGAATA TGAATAACAA
14151 GTTACACACA AGGAGAATGG ATGGTGTATG GCTTTTGTGT TTCTCTCTCT
14201 GCTTTTAGAT CACCAGAAAC TAGAACCTGA GGCTCGGATA TGTGACTTCT
14251 TGAACATATC AAACATCGGT GAGTGCTTGG CCACTGGAGCA TTTTGTGGGT
14301 ATTTTGTAGA AGCAGGGATA ACAGATATCC ACTGCTTTTG TGTGTGGGAT
14351 CACCTCTGTC TGTGGACCTT CACCTGGTGT CTGTTTITAC ATGAGCAGGA
14401 TAGCAACTGT GTCTCAGAAT TCTGGGGCAT TCTAGTTTAG AGACCTGAGT
14451 ATCTGCATCA CTGGGCAACC TTCTCAGGGC TGGGGTGTGA GGCATCAGAA
14501 TAGGTTTCAG ATGCTATTTT TTCCCTTTCT CCTTCTGTCT TGGGCTGAG
14551 GTCCAGGGTC CTCAGGCTGT GAGGTTCCGG GCTCCTAGCC TGCCAGGCTC
14601 CCTCACCAGG GGCCATCCAC AGCCCTCATG CAAGGGTACG GATTTTGTIT
14651 GTGACCTGA AAGAGTTTIT TTCTGCTGC GGTGTCTGC AACTCTGGG
14701 GGTTTTCCATG GTGCTCCCAT TTGTATTCC CAGAGCCAGG AAAGCAAGCT
14751 GCCCCCTGCT CTGGCTCCTC TGGCAGAAGG GATGGCAGGA ACCACTCAGT
14801 ATGGGGAGG AGAAAAAGA GGATTTCTCC CTGCTCCAC CCTGACTGGG
14851 GGGACAGAG CACATTTGTT GTTGTGCTAA AGCCTAGGGA GGTTTGCTG
14901 CCTCAACCCA CTCTGGCTCA GTTTTACTTT GTTCAGCTGA AATGGTCTTT
14951 GCAAAAAGC TTGGCCCTGA TTTGGTCTC CTTCAGAGAG GGACAGAAAC
15001 TGGGCTGGCT GCAGTGTCTG AGCAGAAGCC CCAGTGTGA CTTGAGGAG
15051 AGCAAGGAGC ATCTCCTAGG TTTTCCCTGA AAGCCCTGAG TCATCAGAA
15101 AGACACACG TGTCTGTGCT TCCTCAGCA TGGCCATAAT CTCAGGGCTC
15151 CCACTGTGCC CAGAGGCTG CCTGCTCTGC TCTGTGTGGG GCGAGGGCTG
15201 TGAGGTGACT TGCTGAAGCC TAATGCTTCC TTCAGAGCTA CCGAGCCCT

FIGURE 3E

15251 GGCTTCCAG GTCTGGGGCT AGAACAGTCA AAGTGGCTC TGTCATGGAA
15301 GGGCTGAGGT CCTGCTCTAG CCTCTGGGA GAGGAGCAGC TCTGAGGTAG
15351 TCAGAACGTC AGCTGTGCAG GGCCTTCTAG ATGGCAATCA GCAGCTTGA
15401 TTACACCCGA AGCAGATTGG TTGGGOCAGT GGTGATGGC TTTCCTTGAT
15451 GCAGTGTGTT CTGCAGAGCC AGCACCTCTC AGCTGGTGGG TTCTGGCCCG
15501 CAGAAGTACT GGAGCTCCTA GGTGGTTTCT GAGGTTAGGC CTTCACCTGA
15551 AAACAGCGCA GTGGGGACTG ACATGTGTGC TTGTGTAGGA GAGGGCCCCAC
15601 AGAGGGAAC ACCTAGAACG GCAGTCACAG ATTAGGCATG TTTTGCTTGG
15651 CTGACTCAGT GGCTCAAAAA TATTTTATTT ATTGGCAAT ATTTAAAAAT
15701 GAGATTTCAC ATTTTGA AAAAAGAAAAAT CTATTTCCCC GCCTTTCCAG
15751 TCAGAGGCTT TGGCTCTGCT GAGCCCCAC CTTCATGGC CAGAAGGAGC
15801 TGTAGGAGC GGTGGCTGCC CCTGCAGCCC GCTGGCCACT GTCCCTGTCA
15851 CCCACTATGA GCTCACATTT GCATTACCCA CCTGGGCCCC TGTAGGCCCTT
15901 GCAAGCTTGT GACCTCTAAC CTAGAAGTTC CAGAACAGGA AGAAAAACA
15951 TGTGGGTGAC TAAAGCCACC CATAAGCACA GAAGCATTTT GATGTTCAG
16001 ACOOGGGTCT CAATATCTGA GGAGGGTAAC TTCTTTTCTT TTATGCTCTT
16051 TGTGACCAAC TGGTACAGCA GTGATAATTT GTCTCATGT AGGCAGGAGA
16101 ACAGCAGCTA GGGGTGAGTG ATGCAGGAAG CAGAACCATG TCCACATCAC
16151 CCGGATGCG GCGGGTTGA CCATGGGCGG GTTGACCAGC GATGGGTGG
16201 CCAGGACCG GTACGGGTAT AATGAAGACA ATTGAGAAAT GAGCAGGAAG
16251 GACAAAAATA GAATTCCTAGG TGAAAAAAGC CCTAGGTGTC TTTTATTTA
16301 TTTCTAGAAT TAAATACATA CTTTTTTACC CCATAGACTT CACTCTGTTT
16351 GGTAGCCCTT TACTTTTACC ATCTGCCCTC GGCTCAGAT GGAGGCAGGC
16401 GGAGGACCA TATATCTGG CCGTCTGCTC AGAGGCCAGG TGGGCGACAG
16451 TCCTCTTTT GGCCTCTGAT TTCTAGAAC TGTGCTTCA TTTCTAGCT
16501 GCTCCAGGT CCTAAGGAGG TTGGTCCGAG GACCGATTCT GGGGTGAGG
16551 GTGGGACAG GGAAGGGGGA GTCAAGACTG TGTCTGGGA GCTCCAGCAT
16601 CCGGTGGGA CCAGGCTGT TGGAGATGTG GCGGAGCTGC AGGTCAGGC
16651 GGTGTGGTT GCCATGGATC TGGACCTGGC TTGTGGCAGG AGAGGAGGCA
16701 ATTTTGTGCC CCTAATTCAC TATTCCTCTT CTCCTCCAC TGGCTGTGCC
16751 TTCAGACTG TGACCTTTT GGCCTGGCC TCTTGAATC CATCCAAAG
16801 GAAACCAAC GGGCCAGCC AAGAACAGTG CACAGTGAG GAAGCTAGAG
16851 CAAAGAGCAT GTGGTCAGCC CTGGCTGTGG TCAGACTCGG AGGCACCTGA
16901 TTCAGATGA GCATTGTGGT CTAGGGGCA GTCATGCCA GTTTCCCTT
16951 AATAGCTAGT ATATCTCTG CAGGAGTTA AAAGCCTGTT GGAAGAGTGA
17001 AOCCTGATAT AAACCTCTGA CTTTGGGTAA TGATGATGAG TCAATGTGGG
17051 TTCATAGAG GTAAACAAAT CACCACCTA GTGGGAGATG TTGATGTGGG
17101 AGGACACTG GCATGTGGG GACGTGGGT ATTGTGGAT GTCTCGGGT
17151 ATTTGGGAC ACCCTGTACT TTCCGCTCAA TTTTGGGTG AACCTAAAC
17201 TGCTCTGAAA ATAAAGTTTA TTAATTAAAA ACAACAAAC AAACAACAA
17251 ATGCCGTGTT GGGGTGAAG CACACTGCC AACTCCAAAC AGGCTGGGA
17301 GTGGGCCAG TGGTGGGAG TTGAGAGGAG GAGACGCTGG TGTGAGGTCT
17351 GAGGCTGAA TGAAGTCCG TCTACCTGIG ATCTGCCCTG TCCCTGCTCT
17401 CAAGTCCCT AATGAATAGA CTCGTCTTC CTTCGTGCTG AGCTGCCCA
17451 GCAGTTTGA TCATAGTCTA GCATTGTGGT TTAGAGCAGC ACTTCTCAA
17501 CTTTATGTG CTTAAGACTC ACGCAGGAT CATGTTAAAA TTCAGATTCT
17551 GATTGAGGG GTCTGGGGTA GGACCTGAGT CTCAGCTGA TGCTCATGCT
17601 ACTGTGCCG ATGCCGTGA ATACTTGGAG AAGCCAGTT TTGGCGCTTC
17651 GGAGTCCAT CCAGATTGG GGTTTGAATC TGGGATTGTC TAATTAGTAA
17701 CTGTGACCT TGGCAAGTTA TTTAACTCCT CTAATGCCCT CTCGTGTTTG
17751 TTATCTGGGT CCTTGTGGG AGTGTGTTAG AAAGGGTCA GGCAGGAAG
17801 GGGCTAGGA GGGAGATGAT GAAATGGAG ATTCCAGCC CTAGAAGTGA
17851 TCCTCTCAAG ACCCCAGCC TCGACTCAGT TCACAAGTTA TTCAGCCCTG
17901 ACCATTATCC CTGTAGCCCA GTACCCATTC AGCTAACAGT AAGTGTAGCA
17951 AAGAAACGT TGCAAAATAA AAGAAACATT GAATCATGAC TGAGCAGTTC
18001 CTACATCCCT GCCCCATGG TGGGGTGGG GGGAGCCCTG CCACAGTAAG
18051 CTCCTGGGG GCAGCTCAGT CCCCCAAG CCCCCATGG AACAGGACCT
18101 CCTTCCACT GTGTATTGC TGCAGATATT TTTAAGCACA ACCTTTTTC
18151 AGTGTCTTTT GGAGAAAGAT TTGTATGTTA AAATGTGGCA TATTGTGGG
18201 TGGTTTATA AGAATTGGAA ATAGCCACAA CATTTGGGT GTGGCTATCT
18251 CAGTCTTGA AGACATGAAA TATCAAGTAA AGGTGTGTAG GTGTGTTGGC

FIGURE 3F

18301 CTGTCTCTGTC TTCCAGGGTT TTAAAGAAC AGCAATTAGG TTGTGTGCTG
18351 AAATGCAGTA AATGCTTTAT ACTCCITTC CCAGATCTTC CTGTCTATGG
18401 ACATGGGCTG GCGCTGTGTG GCGCTCATGC CCTGTCTTFA CTCTGGAATG
18451 GGCTGGGTGT CAGATTATTT TATTCCAGC ATCCATAGTC CCTCTGCTCC
18501 TGCTTCACAG CATGACACAG TTGTGCTTAG TTAAGCCATT TGTTGTAATG
18551 CTGGTTTAAA GCGTGTCTTC CCTCTTCGCC TGGCAGCTCC AGGTGGCAGG
18601 GCGGCTCCT CTCTCTACA GCCACATCCA TGGCATGTAC AGGCTGGCT
18651 GCTCGGGGT AGCTGCCAG TGCACATTGT CGAGCCAGTC AGAATGGCCA
18701 CAGGTAGTGG GGACAGATTG GAGCTCCTTT GCGTAAGAA TGTAGAAGGT
18751 GACTCCCAAG CAACTCTGCA ATATCAGGAA TCTTGATGTT GGTTTGTCTT
18801 GCGTTCAAGT CCGGTTCTG CCACTTAGTG TGATTTTGGG CAGGTTTCTT
18851 ATGAGGCTC AGTTTCTCT CCTGTGAGT GGGGTTATTT ATATGTAAGT
18901 AGCTACCTG CAGAGCTGGT GTGAGGGTTC AATACAGTAA TGCAGGTGGA
18951 GCCATGGAA CGATGCCGC ACAAGCAGC CTCAACTAAG TGTAGTTGT
19001 TAGATTAGA TTGTATTAT CAGAATCTCA TGGGGTGGG TGGCTACAG
19051 CTGTGGTCCC AGGCTCTAG GAGGCTGAGA CAGGAGATGG CTCAGACCA
19101 GGATCTCCAG CCCAGGCTGG GCAACATAGT GAGACCTGT CTCTTAAAAA
19151 AAAAAAGAAA TAATGAATCT GCCTGTGCTA AATAGGCACT TAGAATGGCA
19201 CAGTCATTTC TCCTCTGTG TTCTAGTCTC TGTAAATTTT TTTACAAATT
19251 AAAAAAATGT CGATAGCAGT CTTATTCAGA TACAGCTTCC TCCATCCCTC
19301 CTGTGTCTGG CAGGTGCTT GCCTGGGGC ACACATCAAA GCCTGTCTCT
19351 CTGCTGGGTG GCGTAGAAG ATTAGTCTTC CTTTGTGCT CCTTCTCTCT
19401 AATTCCTTTC CCGGCTTCC TCCACCTGG GCCTGTGTG TGGCTTCTCT
19451 GGAGAGGGC AGAGGCCAAT GACTCCATGT CTAGGCAGAG GCGTGGGTG
19501 CTGCATCTCT TGCCCTGTTC TTGGCTTGG TGTGCTGGG GGGGCGAGG
19551 TGGTGTGGG CATGGGGTG TGTGGGCAT GGGGTGGGT TCTGGCTGAG
19601 TGAGTGGGC GTGCCAGGC CAGGCAGAGC TGAGTGGCT CACTTCTCTG
19651 AGATGGTGT CAGCATCATA CCTGCTGCTG TCCGTTAAT TCCCATGCT
19701 GCTGCTGTTA GTACCTTCC TAATGGAGCT GGTCTGTAGC TCTGGGACA
19751 GCTGATTTC AGGGATTAT TTGTATTACA CACTTAATG CTTTTAATA
19801 GCAATTTTTT AATTAAATGG AAAGTCTTT TGGAGCGAG GGAGCAGCAG
19851 CTGAGCAAG ACTCAGGCTG AGGCCCGAC TTAGACCAGA GGTGGCAG
19901 TGAGTGGGC GGAGGCAATG GCAGGACTTC GAGAGGACT GATTGAGTGT
19951 ATATGGAGTG TGCCAGGCT AATTTTTATG GGAGGAGGC AGGGGCTGG
20001 GCTGCTCTC TTCTCTCTGT CCTAAAAGCC CCTCTGTCA TCTGAGGCC
20051 TAGGGAAGCA TCTCTTTTC CCAGGAGAGA ATGTATATAT GATATATACA
20101 TTATATCCAA TAATGGGAG GATATTGGAA GTATCACCTG CCTTTGATCC
20151 GCTTCCAGA AATACAGAGA TTGGGATGG ATTTTGGGG TTGAGTCACT
20201 AGATTAGATC AAATAGTGTG GGTAAATGGA TGCGGAAACA GTCTGAGGC
20251 CTTGGCTCCG GCGTGGCAG GCTTGGAGT CCTCAGTCAT CAAGGAGGA
20301 GAACAAGGG GCTATAGTGG TGGTTCAGTG CCTCGGACT GTGCCGCTG
20351 GGTGTATAC TTGTCTTCT GAATGATCTT GCTTGTGGG GAGGGGACAT
20401 AGGGAAGCAC CTCAGCCTG AGGAAACGTG TGCACTTGA AATGGAAGCA
20451 GCGAGGCCC ACCAGGAAG AGACATGCC ATTTCTTTGT CTCTAGCAC
20501 TGAACCTGTT AGTTTGGTGT CAGGCCATTC CTAAGTGTCT CCAAGGAGT
20551 CACCTGTAC TGCCAAGCT TGGAGCAAAG GTCAAACCA GGGAGGCTT
20601 TGGACAGAA GTTCCCATC AAGAGAGTTC ACCGTAGGG AGGACAGGA
20651 CAGTCAGCA AAGCGGAGT GTTCTGCTAT TAGAATGATG CTCAGGGGT
20701 GGCATTTAAC CCAGAGGTG CTTTGTGGG AGAACTTGA AGAGGAGAC
20751 TCAGAGACT TCAGGTGGT TTTTACCCA AGAGCTTTG AGGCGGGAG
20801 CAGGAGGGA TTCCGCTGC CAGCTTTTC TCGCAGCTG TGCATGCCC
20851 GAGCTTCTT CAGTGGCAC CCTCCCGAC CTGTCTGCA TGTGCTTTA
20901 GGGACATTG TAAGTGGTCT TTCTTTTGA TGCCAGGCT TTGTGCTG
20951 AATATGGGG CTGCCCACT TTCTTTAAG GAAGCAGTGG TGTAGCCAC
21001 AGCTTTTGA GTACAGTAG ACTGGATTCA CATCTTGACC CACACTTAG
21051 AAGCTCTTT GCTTTGTGA AGAGACTTTG TGTCCCTGAG CCTCTGGTG
21101 CCTCATCTGT AGAATGGGAA TAACATTCAT CTCAGGTGTT CTAAGGAAT
21151 AATAAAGTCC TCAAGGCGAG GCACTCTGT TGTCTCTCT GAATCCGCT
21201 GCTTAGGCTG GGTCCAGCA CATAGTAGGT GCTTGATAAA TGTGTGAGA
21251 ATCAGTAATG TATGCAAGAG CCTAGCACA GCGCTGGCAT AGTAAGCACT
21301 TAATAAGCTG TTAATGTGT CATTGCTGA ATGTGTGCT GCGCTCCAG

FIGURE 3G

21351 GCTCACCATC CATTATCCTG CACCACGTCG CTTCCTGCTG AGCTCTGCTT
21401 TTCCACCTTC TTCCCCACCC CTTAGTTCCTG CTCACATTTA CTGCTCTGGA
21451 AGAGCTCTCT GGCTTTCCCA TCIGGTCATT GTTGTCCTCT GCGTCAACA
21501 TTGCTAGGTG CTGCTCAGGC TGCATCTCAC CATGTGTCAT CATATCCAG
21551 GACCACCTTC TGGGAGACCA GCGCTCTGGG AAGGTTCCGG CTTTCTCTCA
21601 TCTTGACTTC TTAGCCATGA AGCTTTCTCT TCTTGCTTGA GTCTGAGGTG
21651 GCAACACAGG CGCCAGGCTC TGGCTCCAGG GCTGCATAGC CTGCGACTGG
21701 GGGGCACTGG GCACGTCCGC ACTTCCCCC ACTGCTCTTT CTGGAGAGCC
21751 CTGTGAGCCG GACAGGATGG GGCAGGGGTG GGGCTGCTGA GGAGAAGCCT
21801 AGGATTTCCA AGTTTCTCTT CTGTAACTT CTGTCCCAT CTCTCTCTTT
21851 GCAGTGGGCC TCCATGACAG TATTTCTGAA GAAGGTTTC ACTACCTGTT
21901 GTTGAACCTG TAAGTGCCAC TTTCGAGGG TGTGGGGGCC TTTCCTCTTA
21951 GCTGACTCAA AATGAAGGCT CAGGAAGGGG CCTAAACAGG CTCTCCAGCC
22001 TCGCCCCAGG GCGCCCTCTT TTGTCGAGG GAAAGGATTT GACTGGGGCA
22051 GATTGCTGCG CCCACCAAGG GGGTCTCCAT GTTCCCCAG CGTCCCCCA
22101 GGGCTCTGAA CCCCAGGACA GCATTCCTCT CGCCTCTCTG TTCAGCAGCA
22151 GCGCTTGCAC AGATGCCCTT GTCTGTGTTT TCAGTGTGCT GTCTTAGTGT
22201 AAGAAATAAA AGACAGCTCT TTGCATGACC TTAATAATCC TGAGAATCA
22251 GAGGTAGCTT TCATTAGTGG GAAACCCAGC TCCATTGGAT TGGGTCTCTC
22301 CTCACGTTG GTTGTGGTTT AATGTCCTAA AAGTGGCTCT TACCTCTGG
22351 ACACCTCTCT CCAGATCTCT CAGGGTTGGG TCTCTGTGTC ATTGTCTCA
22401 TTACTCTTCA ACTTCAGTAG TAGCTCTGTC CTTCCTGGGC AGCGATATTT
22451 TAGTGTATAT GTTGGTCTCA AAGCTGTGAC TTTTGGGGTA GGTGACTGT
22501 TTTCTCTTAG ATCCCTGTAT CTTATCTCTT GCGTACTAT TAGTGAATCT
22551 GTGCATTTTG GAAAAAGAAA TGTCCGGAAG GAAGGCAAGC CCGATGATAC
22601 CTCAGGAGA ATCCGGGTGT CACTGAAGGA TCGAGTGTGT TCTGAGCTCT
22651 CAGATGAAT GCATGGGGAG TTGGGATTTT TCTGAAGCC ATTCTACAGG
22701 GTGACCTGT TTTCTCTTGG ACATGGGGT TGGACAAGG ACCCTTTCTG
22751 CCTCTGACC TCTTCTTCCC GTTGGTTCGA GTGTACCGG CCGGGAGCTG
22801 TTTGAAGACA TTGTGGCCAG AGAGTACTAC AGTGAAGCAG ATGCCAGGTA
22851 GGATGAGGGC CCGAGAGTTC AAATGTAGCT CTGGAGTTTA GGAATGAAGG
22901 AAGTCTTGGC CACCTTGGGG GTCCAGCATT GTACCTGTTT GAATAGTCTT
22951 TGGGGAAGCT CAGAATAGCT CTTGTCTGCA GAAAGATCT GTTGAAGCTG
23001 GCTAGGGCTT GCATAGTGTG GGTGATATTA GAAGTAAAA ATTACAGACT
23051 TCTTAACCCAG GCGCAGTGGC TCATGCCCTG AATCCAGCA CTTTGGGAGG
23101 CTGAGGCAGT TGGATCACTT GAGGTACAGG GTTGGAGCC AGCTGGCCA
23151 ACATAGTGA ACCCTGTCTC TACTAAAAAT ACAAAAAAT TAGCCGGGTG
23201 TGGTGGTGTG TGCCGTGAAT CCCAGCTACT TAGGCGGCTG AGGCAGGAGA
23251 ATCACTTAA CTTGTAAAGG AAGGTGTGAG TGAGCCAGA TCATGCCAT
23301 GCATCCAGC CTGCGTAAAC GAGCGAGACT ATGTCCCTCT CCCCCCCCC
23351 CAAAAAAAAT ATCACTTCCA AATGAATGTT TTACAAAGCT TTTCCAAGTC
23401 TCTTTTACCC TGTGACCCCA GAAATACTTT TTTTGTGAC TACCATGTAC
23451 TCGCCACCAT GCGCAATGTC CCGCTCTGCC CTTTCTCTTC CTTTGAACAA
23501 TTTCTGGTGT CTCAGGCCAC TGTGCTGAGG CTCGGGCTAT ATCCAGAGGT
23551 GCAGAAGACA TGGTTCTGT CTTGAGGGAG TGGAGAGTTC TGGCTGATA
23601 ATCCAACCAT AGAGCCCGGG GAGCTTTGAG CCTCTGTAC CTTGTCCCTA
23651 GACCACCATG ACCAGCCTTG CCGTGGGGCT CCTCCACTT GAGGACCGTT
23701 CCGCGGCCAC ATGCCCTAGC CTCGCCCCC CCTGGAATCC CTGGTGGCTC
23751 CTTCAACCCG GCTCTCAGGT GCGTGTTCAG CCTGTCTTTC CCGCTTGGC
23801 TCTTCCCCCA GCGTTGCTTT TCTCGAGGGT GATGTCCCTA CAACCTGGTT
23851 TTGATCATCT TGCTGACGCT TTATCTGGCT TATGTGGCAG CTCGCTGCTC
23901 TTTCTGAGAG TGGGGGAGTG CAGCTTCTCT ACGAATTTCT CAACCTGAG
23951 AGGCAATGT TTGCTGATCA ACTTCAGATG CTTGAGCTCT GGGAGAATT
24001 CTCAGTGGG GAGATGAAT CCAGTGGCAG CAGGGGAGGA CGAGGCTCTG
24051 GGACGGAGGA GGCAGTATG GCTCAGGGAG CCTGCGGGGA GGAGGGAGAG
24101 CTATAGGGAG GGGGCCCTGA GGGGGGGTGA CTGTACCACT GGGCTTGGCC
24151 TGGCTCTGCT GGCACACTTC GCACCTTTGC CATTTTGGC CAGAAGGCGC
24201 TCCCTGCTAG CCGGCTCTG TTCTAATTAT ACATCTCTGT GGAGACTGCG
24251 CTCTATAGCT CAGTCTTAAA GTTCTGTGTG CCGACTCTTG GCGTGTGTCC
24301 TATGGGGAGG CCGAGTTTC AGCCCCAGG GACCCAGTAC GACCCCTTGG
24351 TTTCTGTGGC ATCCCCAGCA TCAGATTTTA GGAATAGTAA GTCCAGGCCA

FIGURE 3H

24401 CCCAGCCCCA TACACTGGGA TGCTCTGCAG ATGTGCTTAA TATACCAGAT
24451 AGTGOCTGAT GACGGGGGTC TATATCTTAG GCCAAGTTOC TCAGCCTTGG
24501 TGCTACTAAC GTTTTAGGCC AGGTACTTCC TTGTGTGAG GCCTCTCCTG
24551 TGCATTGTGG CAGACATTTA GAAGCATCCT TGGCCTCTGC CCACCAAATG
24601 CTGGGAGCAC CCTCTCTCCA GTGTGACAA CCAGAAATTT CTCTAGGCAT
24651 TGCCAAATGT CCGCTGGCGT GGGGGGGGGC GGGCGGCAAA TTCATTCCCA
24701 GTTGAAAACC ACTGCTCTAG ACTGCCCCCG CTCCTGTGTA GGAGTTTGAT
24751 GACAGGATG GCAGGATGGT TTGCTATGIG GACAGTCTGA TTACGTGTG
24801 TGACTGTGGC TGGGCGCAGT GGCTCACGCC TGTAATCCCA ACCTGTAGAG
24851 GCCAAGGTGG GTGGATCACT TGAGCTCAGG AGTTCAAGAC CAGCCTGGGC
24901 AACATGGTGA GACCTGTGCT CCACAAAAAA ATACAAAAAT TAGCTGGGCA
24951 CGGTGGCTCA TGCTGTGTGT CCGAGCTACT GGGGAGGCTG AAGTGGGAGG
25001 ATTGCTTGAG CCCAGGAGT CAAGGCTGGG GTGAGCTGTG TTACGACAT
25051 TGCACCTTAA CCCAGCAAC AGAGTGAGAC CCTGTCTCAA AAATAAATA
25101 ATAAAAATAA TTTGGGTTTT TTCTCTACG CAAAATCATC AGAAGTGTCT
25151 CTTAAATGCC CTGTTTGGAA GCTCTTAAGT ACATGTGTTT TTAAAGGTAT
25201 CTTTGTACTT GTTTTAGCTG CCTTACTGGA TGCCAGACCT CAGGGCAGCT
25251 ATTGGGTCTT GTCCATCTTC ATTATCCTAG GCACTCAATA AACATTTAGG
25301 GAAATGAATG AGTGACCCCA CGCCAAAGT AGCTTAGGTT GTTTAGTTGG
25351 ACTCTCCTTC CTAAGTTGCC AGCACAAGCT TCTTCTCCAA GAACAAAGTT
25401 ACTGTATGGA GAAAGAGAAA GAAGGAAGG ATTGGATGCT CTCCTCTTCC
25451 TCAGGATTTCT GGCCTGTCTC CTGATCTCTT GGAATGAGT TGGTGTGTG
25501 AGACCTTTCC AGTCAAAAGG GGGTGAGAG AACCCTTTCT AGCGGTGATC
25551 CTAGAAAAAC CATGTGATCT GCTTGGGCTT GGGTTTCTTC TTCTTTTAAA
25601 TAGGTTGAAC AAGATGATGT GCAGAGTCTA AGGTTCCAGT GCGCGTTAAG
25651 TGATTTCTCT TGAATCCGIG GCGCCTTGTC ACATGCCCTA GTCTGCAGCA
25701 TGTGGTGTGT GATGTGGATG AGGTGGTTTA ACCCTGGGCT AACATTTCTT
25751 TTCTCTCTGC TTTTTTAGCC ACTGTATACA TCAGATTCTG GAGAGTGTTA
25801 ACCACATCCA CCAGCATGAC ATGTTCCACA GGGACCTGAA GGTACTACCC
25851 AGGCTCCCTT CCGTGCTCTT GCTCATGAAG TGTGTGGGCC ACCTGGTGCC
25901 AGATAGTGGT ACTGCGTAGG CCAAACTAG GCTTCTCTG GGTGCAGGG
25951 TGGGTGCTCA CAAGGTTCTC TGTGTTTCTT CTGAGGCTG AGAACCTGCT
26001 GCTGGCGAT AAATGCAAGG GTGCGCGCT CAAGCTGGCT GATTTTGGCC
26051 TAGCCATCCA AGTACAGGGA GAGCAGCAGG CTTGGTTTGG TAAGGGTGAT
26101 CCTGTCTTCC CGGAATGCAG CCGCGCGCT TCTCTCTCTT CCTGATCTGC
26151 CTCTCTCTAT TAGAATAGA AGCCAGACCC TTAATGGTCC TGGCCTCCGA
26201 GATCTCTCTT GCGGTACGC GACTCAGTAC AGTAAGTCTA GCTGTGTCTA
26251 GCATGCTTTT CTGTGCTGCT GTGGGAAGGA GCTGGAGTTC CTGGTAGCCA
26301 TACGGCTTTG CCGTCTGGT CAGATTCCAG GCGCTACAG AAGCCAGGCC
26351 TGTACGCTCT TGTGCGCAT GTGCTGAGAG TTTATGTAGC AAAAGCAGCA
26401 GGAATAAGAT GGCACCTGGG GGAATGGCT GGTGTGGATT TAACGAGAGA
26451 GAAAGTGGT TCAGTATGCC TCTGCGCTCT CTTTGTCTAC AGGTTTGTCT
26501 GGCACCCAG GTTACTGTGC CCGTGAAGT TTAGGAAAG ATCCTATGAG
26551 AAAACCTGTG GATATCTGGG CCGCGGTAA GCCATTCOA GCTCTCAGC
26601 TTTTGGCTGT TAAGGGCGCT CAACCTCCA TGATGCCAG AAGAGGCAT
26651 CGCTATCTCT TGCAGGTAC ACAGTGCTT GGTGTATGTG AAATPATGGT
26701 GTTTGCGCCT GGGATGGCTG TTCCATCAC ACGCTCTCC CTGGTACTT
26751 CTGGGATGAC ATGTATCTCT TCTGTGAGAG GGATTGGCC ACGCTTAGA
26801 GGATGGGTG TGCTAAAGA AATCCCTGGT GTGACTTGGT GACGTGAAGT
26851 GTGAGGCATA GCAGGAGGGG CTGGTAGCAT AGCATTATCG GCTGGCATCC
26901 ACTTCTGACT CTGGTATGGC CCGTGTCTT CTAGGTGGCT CTGAGCCCTG
26951 CATGGTTTTT CTGGTCTCT CAGGAAGTA GCGACTGAC CCGCATGACC
27001 TGTGTGTCTT GTCTGTAGG GTTATCTCTG TATATCTCTC TGGTGGGCTA
27051 TCTCTCTCTC TGGGATGAGG ATCAGCACA GCCTATCAG CAGATCAAGG
27101 CTGGAGCTA TGATGTAAG ACCAGAGAG CCGGAGCCA GCGCAGGAG
27151 GGCAGATGTC CTGCTCTCTG GCTCTGTCTC AAGGAGCAG GCTGTGTTAG
27201 TGTGTACGT GATACGGGG TGTACGGGA CTTTGAAGC CCAGGAATGG
27251 GCATCCAGGG CCAATTTCTT GCGACTCTAT GTCCAGGGA GCACTTTCT
27301 TTTGCACAGC CTCTCTCATA ACTAAAATTG AGGAGTCCAC TGAAGTCTTT
27351 TGATCTTTAC TTGCAAGAA TGAGCGGCC TCATTGGTGT GCTGTGTAC
27401 ACAGGGACAA AAGGCTGGA GACTCCTCTC ACTGAGTGG CACCTTGGAC

FIGURE 31

27451 ACATITGCTGA GCTCTGTTC CCTCCTAAGT ATAGAGCTGG GCTTAAACCA
27501 GAGAAITGTT GAGTCCCTTT CCCGCTCTAA TCTGATGFTC TGGCAITCTA
27551 AACATGACTG TTCTGTCTGT CTTTCCAAGT CTTTAAAGTTG ACACAGGTTT
27601 TGGAAITAGCC GCAGGGCTTC TCCAACCTCG CCAGTCACAG CTTTAGGTAC
27651 CACAGAGTAT CCAATTACA GGAGTTGAGT TGAAGACAGA ACCAGTGTGT
27701 CAGGTTATGA AGCTCACAA TACCACATTC TTCTCCCTAT TCTGCTCCT
27751 TAGTTCOCAT CACCAGAATG GGACACGGTA ACTCCTGAAG CCAAGAACIT
27801 GATCAACCAG ATGCTGACCA TAAACCCAGC AAAGCGCATC ACGGCTGACC
27851 AGGCCTCTAA GCACCCGTGG GTCTGTGTAA GTGTCTTTGC TAGTGGCCAA
27901 GGAGCTCAGG GGTGTACGCC TTCTGTGTGC CCTCGGCACC ACCCCCTCCT
27951 TCTTAACCAG AGAGATTCTT TCTGGGCCCC AAGCAATAAC TGAGCAGGCG
28001 GGCAGAGGAC TGTGTAGGGC CAGGGTCAAT AAATGTACCC AGGAGAGCTC
28051 GGGAGGCTGA TGGGGCTGGT GGGCCACTGC TCTCTCTCC CCCACTCATG
28101 CTTGTCTAGG TGGGATTGGT TCTGTCTTGT GATGAGGGCT CAGGTTGACC
28151 TCTGTGACTT CCAGGTAGCC GTGTATAGAA AGCAGCTGCG AAAACCCAAA
28201 GTGAATTCCC AAGCTGGGGT TCATACTCAG ATCTCAACTC CACTGGAGTG
28251 GTGACCAAGA TCCAACAAAT CAACAGAAGG GGTTCCTGAG TCATTAAAAG
28301 CATAAAAGCT GAGGCATAAA GCTCTCGCC TAAAGTCCCTA GGAGAGTCTT
28351 CTAGGCTATC AGTGTGGGTT GAGTACTCTT GTTTTATAC ACAATTCCTT
28401 CAAGCTGAAA TATCAACTTT CAGACAAAGA AGAGGATTTG GTAGAGTTAG
28451 GCATCTTGAC AACACGAGG CATTAATTAT CTGTCCATTC TGTGTTTATT
28501 AAATACCTCT TTGGTGTCTG TTACCGTCTG GGTGCTGGAG ATACAAAGAT
28551 GAATGAGGCA TGGTCCCTGC CCAAAAGAT CATCTAGGGA GACAGGCACT
28601 CAAACAGGCA GTCATGTATC AATGTGACAA GTAGGTACAA GAATCTAATG
28651 AGAGTACAGG AGTCCCTACT GTTCCCTGGT GGTGGTGGGG TTACTGAAGG
28701 CTGCACGGAG GAGGTGACAC CCGTGTGCTT GTTCTTGGCA AATAACGAGG
28751 TCTTCAGAAC GTTAACCTGC AGACAGAGTT TAGCACAGTG AGAGGTTATG
28801 GGAACTATG GTGAGTTGAA GGAATGTGA GTTGTTTGGT TGTGGATGAG
28851 GCTGCAATA TCAGATGCA AGAGAATGGG GCAAAAGATT CCGTACATA
28901 CAAGTTTCTG CCTCAGGAGT TTGGATTTTA TTCTGAAAC ATAGGGAATC
28951 ATTTAAGGGT TTTAAAGAAG AATGAAATTT GCATTTAAGA ACACITTTGA
29001 AGTTGTGAGG AAATGAATTG CCAGGCATGG TGGCATGTGC CTGTAGTCTC
29051 AGCTGCTGGG GATGCTGAGG CAGGAGGATC ATAAGCCGAG GAGTTTGAGG
29101 CTGCAGGAG CTATGATTCG ACCTGIGAAT AGTCATTGTA CTCAGCCTG
29151 GGAAGATGG TCAGACCCCA CCTCTTTAAA AAAAAAAAAA AAAAAAGAAG
29201 GGAATTGAAA ATTTTAAAAA GAAAGGGCT GGAGACAGAG AGCTCAGGAA
29251 GCTTTTAA TAAGTTGAAT AGTCTAAGCA AGACAGGAGG AGGTCTCAGC
29301 AGAGGTAAG GATGGGGGAA TGTCCAGTGT GTTGAATTC AAGAGATATT
29351 TGACAGAAC TAAAGGATTT AATCTCTCC AGTTGGATTT GGGGGAGCA
29401 AAGAGAGAG AGGCCAGGTT TCAAGTTGAG CGGAGAGTTG TACCCTCACT
29451 GACCCAGAAG AAAACCAGAG GAGGAGCTTG TTTGTGAGC AAGACGATGG
29501 TTTTCTCTTT TTTTCTTTT TTTTGAGATG GAGTCTCCT CTGTGCCCCA
29551 GGTGGAGTGT CAGTGGGGG GTCTCACTGC AAGCTCTGCC TCCGGGTTT
29601 ATGCCATTCT CTGCTCAG CCTCCGAGT AGCTGGGACT ACAGGTGCCC
29651 GCCACCGGC CCGCTAATT TTTTGTATT TTAGTAGAGA TGGGGTTTCA
29701 CCGTGTAGT CAGGATGGTT TCGATCTCCT GATCTCATGA TCCACCCGCC
29751 TCGCTTCCC AAGTGTCTGA GATTACAGGC ATGAGCCACT GCGCCCGGCC
29801 AAGATGATGG TTTTCATTT GTGCCCTG AGTCTGGCAA CCTCCAGCCA
29851 GACACATTC GTGGGTGGTT AGAAATATGG TCTTAGAGAT TAGAAAAGAA
29901 GCTAAAAATT GGAATCCAC ATTGTAGTCA TTTCTGTGTA GTTGGTAGTG
29951 AGGCTGTAGA AATAGCCTCT TCTATGCTG TAGATGGGCC TGTCTCTATG
30001 CTGGTTGAGT TCTTACGGTG AGCTTCTATT GGTGTAGTA GAGAAGAGAC
30051 GGCCTACTA CACCAGCATT TAATGATAGG GAGAGTTAGG GGGCCAGCA
30101 AAGAGCACTG AGAGTGAGAC CTCCAGAAG ACCCAGAAGC TAAGAAACAG
30151 GGGTCTCAG TAAGGGAGCG TCAGGAATCA GATGAGAAG AGTCCCTGAT
30201 TAAGTTGGGG AAGAATCCC TGCTCTGAC CATTAGATGC CATTGTTTCA
30251 TCAATTCCT GAGACAGTGG AGAGAAAGAT GAAACCTGT TTTGAGTGG
30301 ACCGAAAGGG AGTGGGGTG AGGAGGGGCA TGGGGAGCTA GGCATTGAGG
30351 TGGGAATAA ATGGTATAC TTAGATTAG ATGGGCCAGG GGAGCTTTTA
30401 ATGTAAGGCT CACACCTGTA ATCCAGCAC TTTGGGAGAC CAAGGCAGGC
30451 GATCATTGA GGCCAGGAT TCAAGACCAG CCTGGCCAAC ATAGTGAAC

FIGURE 3J

30501 TCCATCTCTA CTAAAAATAC AAAAAATTAG CTGGGTATGT TGGTACACAC
30551 CTATAATCCC AGCTACTTGG GAGGCTGAGG CATGAGAATC ACTAGAATCC
30601 AGGAGGTGGA GGTTCGAGTG AGCCAAGATA ATGACACTGC ATTCCAGCCT
30651 GGGTGACAGA GGGAGACTCT GCGCTAAAG AAGAAAAAAT TTCCTTTTAA
30701 AGATTATATT GGTACGGAGC GGTGGCTCAC ACCGTGTAGT CCAGCACTTT
30751 GGGAGACAG GGTAGGTAGA TCACCTGAGC CCGAAGTTT GAGACAGCC
30801 TGGGCAACAT GCAAAACCC CATCTCTACA AAAAAAATA CTTTAAATAT
30851 TAGCTGGTTG TGGTAACTG CCTAGCTTAC TTGGGAGGCT GAGATGAGAG
30901 GATCACTGGA GCGTACAGAG GTGGAGGTG CAGTAAGCCA TTATTGTGCT
30951 ACTGCCTCC AGCCTGGGCA ACAGAGTGG ATGCTGTTC AAAAAAATA
31001 AAAAAATTTT TGTTTTAAAG AGAGGCTTAA CTATAATCTA TAGAGAAGAA
31051 TCTAGTCCAG AGCAAGAGT TGAAGATCCT TGCTAATGTA GGAGCAAGAG
31101 GTTTGGACAG CAGAAAAAGA GAGGGGGCTC CTGAGCCAG GCGAGGGGT
31151 CCATCCCGGG GATGACCATG ATCCCTCTGA GACTTCTATT AGTGTGGAGG
31201 CAGGTGAGG TCGGCTGTG AGTGAAGTC TGAGCTGAAA GGGGTCTTG
31251 CTGATGACCT CTCATTTTGC TTTTGGAGAA ATTTACACCG AGGAGGAGGT
31301 AAAATGAGAG ACTTGGGGA GGTAGAGAAG GTGGGGAGAG TTGCTCCGG
31351 ACCTGGAAAG AGTGGGCAA GGGTGAAGGA AAGGATGGA GGAGGCCCCG
31401 TAGTGTGGT GGGCACTGG CTGAGGTGC CAGGATTGT TTTCTGACA
31451 GGTGTGTGA GACAGCAACA GCAAGGGAG AGGGCAAGCA ACCTGAACA
31501 GGCAACCAG AATGGGGGA ATATTCTGTT CTGGGGTAT TTTTGCAGGC
31551 CCTACCTCT GCGTCCCTG GTGTCTGAG CCGCTGAGGA CATCACTATA
31601 TTCTGAAAT ACATAATGAT GCTGGTATG ACAGCTGAGT CATGAGGAA
31651 GTGTAGACTG TGTCCTATG ACTCTGTTA AGGAGGCGAG GAAGTATGA
31701 GTAAATACAT TGAAGCAAA TTTCATCCA AAAAAGGGG GGCACAGTG
31751 CTCACCTTG TTATCCAGG ACTCTGGGAG GCGAAGTGA GCAGTCACT
31801 TGAGGTGAG AGTTCAGAG CACAGGCTG GCGAATGGA CCAACCTGT
31851 CTCCTACTAA AATACAAAA TTAGCTGGT GTGGTGGAT GTGCTGTAG
31901 TCCAGCTAC TCGGAGGCG AAGACAGGAG AACCTGAGAG GCGAGGCTA
31951 GGTGTAGCG AGATTGCACT ACTGCCTCC AGCTGACTG ACAAGGCGAG
32001 ACTCCATTC AAAAAAATA AAAAATTACA TCCAGATGA TGAAAGAT
32051 TGATGCTTCA AGGTGAGAT CCTTAGCTTC TGGGATCATG GCTTCATTC
32101 GCACTGTCT GGGGTGTGT GAGAGGGGC TCTTGGGAG AAGGAATGTC
32151 CTCTGTAGAG AGCAGGAAC CTGCGTCTT CTGCTGTCTG AGCATCTGA
32201 ACCGATGAG TGCTCAGTAA ACAGCTGCT AAGGAGTGA TGAATGAGGA
32251 TCACAGCCC CAGGGTACT TCTGTCTCG TAGCTCTGT TTCCCAAGGA
32301 AGAATAGGAC GGTCTCTAG CAGCCGCTT AGCATCCGT ATTGGTCTT
32351 CAGGTTCATG TTGTCTTAT GTAACTTGA GTTTGGGTA GTGCTTTAT
32401 TCTAAAGCG TTTTCAATC TGTAACCTA TTTCTCTTC AGACCACTC
32451 TGGGGTGGT GAGTGCATGA CCGTGTCTG GGCATGGTAT CGGTGCCAGG
32501 ACTGTGGGAG GGCAGAGGA TCTGGGCTG GGTCTATAGC CTGTCTGTT
32551 GGTTCCTAG AACGATCCAC GGTGGCATC ATGATGCTC GTACGAGAC
32601 TGTGGAGTGT TTGCGCAAGT TCAATGCCG GAGAAACTG AAGGTGAGT
32651 TGTGTTCTAG GCTGCCAGC TCTTGACAT CATGCCCTG ACCAGTGTG
32701 CTCTGCCCC ATTTGAGAAG GAAGCTTCCC TCTGGCTGG AGCTGGGCTC
32751 TGAAGGTGT ACATGTACA GGGGAGGGG CCGAGAGGC TGAATCTTC
32801 AGGCTCTAGC CAGGACCTG CTTTGCTGA GACGAGCTG CCGTTTCTA
32851 GGTCTCTAGT GAATTCACAG GACCTTCTC TTTCCCGAG GTGCCATCT
32901 CAGGACATG CTGTCTCTA GGAATCTCT AGGTATGTTT TCCAGCTGT
32951 GTACTTTATG TATGCCAGG TGAGTGGAT AGGAATGGG TGTGCTATC
33001 CCGGGCACCG CTGGGTTCCT TCGGGTCTT GGGCACACC TTGACCGGG
33051 CGAGTGAGGA TCTGTGTTG AGGGGCTGCT GCTGCTGCTG AGTCTGCTC
33101 CTGAGATTC GGGGCTGGA CTCACATTTG TGAATGTTT CCTAGAATT
33151 CCAAGAGT AGCCTGCCA ACTTGTCTAG TACCTGTGT CTCTGGATC
33201 TTATTTAACT CTCGAGAGC TCTCAGCACT TTACAGATT TAGCATCTT
33251 AGGATCTTGG AGGATGTGCT GGGGAAGAA AAGAGAGATG AGGTACAGT
33301 AGTCTCTCA ATTTGCAAT TTGCCAAT CATTTGCTG CTGGGAGAT
33351 CTCTTACTTC ATTTGTGCA AGTGGAGAT ACTAATAGAA ATTATCCAG
33401 ATGTTTAAAC CTTTGTGCT GACTGTGCT TAAATAGTC CCTGAGATC
33451 TAGCTATAAC AGTGAAGAA TAAAGACCAG CAGGAGAGG GGAAGGAAC
33501 TTGCTTAAAT TTGCATAAG AATTGGGACA GGTGGGACA ATAATTTGTA

FIGURE 3K

33551 AATCATACTT GACATTATTT TTTAAGATGC AAGACACTCC ACTCCCCCTCT
33601 TGCCCCCACC CTCACCCCAA CCCCATTAT TGTTTGGCTT CAATTGGGAA
33651 GCACAGTGGC TTTTITGTGA GGAAAAGATT AATGTGAGA CTGAAGACAG
33701 AGAGGGCTCT GCCCAGCTTG CCATCTCCCC CGGTCTCTCC TCCCTCTAAC
33751 CCGTTGCCCT ACTGTTTTGG TTCAAGACCC CCCCCTCTCC TTCCATAAT
33801 AAGACTCCCT CCGTTGCTTC CCGTCTGCAC CACCATGGAA AGGGGGTGT
33851 GTGGGAGCCT AAGCCACCAC TCAGTGGGAG CCCTTTCTGA ATACCCGTCC
33901 TGTGGGGCTC GCGTGGGCTG GCTCCAGGTA AGCCAGGGGC CTGGGCTGT
33951 AGGATGCTGC AGGCAGGGAG CCTAGGGCTT CGTGGTGTAG CCGAGAGCC
34001 ATGGAGCTCC GGAAGGCCAG GCGTGGATAG TGAGCCCGGG GCTGGTGGTG
34051 CCGTGGCTTA GGCGTTCTCC TTTGACCCTG GTTTGGGGCT TGATCTGTG
34101 TCATGGGTAC CCAAGAGGG CATACTGTGG TGTGGCTCCA CCGTCTGCAG
34151 ATGGGAACAG GGAAGCGTGG CTGGCTGCGT CCGGTGGAGT TGCAACTGTA
34201 GTCCACACT TGCTTCTTGT GCTTTAATGA CGCAGCTTCT ACTTTTGGG
34251 TCTACGAGCT TTTCAGAGG ACATTGAAGG GCGTTTGGT GTTGGCCCTA
34301 GAGCGAAGCT CTGTCTCTTC TCCCTCTCTA GTTGAAGAAA TGTGAAGACA
34351 GTCTGTGCT TCTCTTTTAG CCGAGCCAGT CAATAGCAAG GCGCCGTCT
34401 TGAGAGCCCG GGCGTCCACA TCAGCCCTCC CCGCAATTTC AGGAACTGG
34451 CATCTGGTTC TCAGGAATTC GGGTGTTAGG ACAAGCAATT TTATTCATCC
34501 CTGTAGAGCC TCCTGTCTTT ATTGGCCAGA CCTAGACTGG CCGTTGAGCT
34551 CACTTTGGCT TGGGTACAGG GAGACAAACA ATGTGTCAAG CATTCAGGA
34601 TGGCTCTTTC TGCCCTGACT CTGGGACAGG TGAGGACAGA GTCTGTCCGG
34651 AAGCTTCTGC AGAAAGAGGT GTCTATGGAT GCAATCAAGA AGGAAGGGCA
34701 CCGTGTGTTC TCTCTAGGGC TGTTTTGTGA GTTGACCTCC AATAGGAGAT
34751 GTGGCTTATC CTGGACTCTA CGAGTTTGGC TAACAGCGAA TCGGGCCCTC
34801 CAGAGTGTAT TGCTTCAGCA GCGTTTGTTC TCTTCTCAG GGTTTATTTT
34851 TTTGGGACCT TTCACTCAG CACACTGTGA CACACAGCT GAGATGCTG
34901 CCGTCTCTGG CTACCTCCCT TAAGACAGGG ACCGTGTCTT CTGAGGGGT
34951 GGGGGGCATG GAGCTGGGGC CCACAGTAA ACTTAGCTGC ACAAGGGCCA
35001 CAGACCTCC CTGGGACCC CAGCCAGTTC CCGTCTAGT GTGGATGTA
35051 GAGAGGGGAG AGGGCTGCTC TGCCGCCCGG GCACCTCTAT CGTGGGCTCA
35101 TTTAGCTTCT AGGGAGGGAA GGACTAGAAG GGAGGGGCTT TCATCACAGC
35151 CTAAAGCTAG GGCGGGCTTA CCGCAGAAGG GGCACCTGCC TCTCACCGGC
35201 TCAGGCATTT CGCTGTGGAC CCGCTCTCGG AGGGGGTCTT GAGACAGGCA
35251 CTGAGCCCT CTCATCTGG TGGGGACGCA GTGTTCCTTA TGCCCTGGCC
35301 CAGCCCGTTC TTCCAGGGC CCGAGACTGC TGAGGGCTG CCGTGGCTTA
35351 CCGCTCAGC CTGCCCCTGG CGCTCCGCTC CCGCAGCTCG GCTGGCTTGG
35401 CCAAGCCGCC TGCGCTGGC CTGCGGCTGG GCGATGCTGG CTGTGACGG
35451 CCGGTGTGCT TTGGGGGGCT CTGTGCACCT AGAGACTGTA TCCCTCAGT
35501 TGCGAGGCTG AGCTCCGCC CCGCTCTGCC TGCCCGGAGC GCGCGGGCC
35551 TGCCCGGGCA AGGTACGTTG CATGAGTCTT CCGGACCGC CTGCTTGGC
35601 CCGCTGCCAC CCAACAGGA GCGCCAGCAT GCGGGGCCA CTCACAGGG
35651 AGCGAGTCC CATGCTTGG GCGTGAATG GCGATGCCAG ACAGACTACC
35701 TAACTTGGCA TCTGCAAGG CATGTTTGT ATTGAGCCCC CTAACAGCC
35751 ATGATGCTG GCGCTTGGC AACCTTCAGG GCGCAGTAGC CTGGGGCAT
35801 GGAGCTGGGC AGCGGAGCC TTGCAAGAG CCGCATGCC TGGAGGGCT
35851 GCAGCAACA GTGGGCCCTC AGAGACAGTG CTGGGCATTG CCGTGAAGTG
35901 CCGGTGTCTA GCACTAGATT TCCGAGCAC TGTTTAAGAC CCAACAGAG
35951 AGCGGGCTC CTCAAAATG TGAAGTCTGG CGCTTGTGG CCGCAGGTC
36001 TGAAGGCTC CAGAGTGCAG AAGCCTCAGA GCGAGCTGTT TCTGGGTTCA
36051 CATCTAGCT CTGCCACAC CTGAGCGAGT CACCCAGCT CCGCAGCT
36101 TAATCTCTCA CCGTCCCAAT GGGATGATA AATAACATGG TGGTGTCTAA
36151 GATCACCTG TCGAAGGCTC TCAGCCCTGC CTGTGCAGTA CAGCTGTAC
36201 CTGGAGCTC GTAAGAGTTC CTAATGCCAG GACCCACCC CAGACAATA
36251 AATCAGACC TTAGGGATAA GATAGGTAGT ACGCTTTTTC TAAGCTCCA
36301 GGTGATCTA GTGGGCAACC AGCGTTGAGA GCTGGCTGGT GAATGGAAAG
36351 CACTTAGACA GTAGGCGTTC AGGCACAGGA GTACACAT TTAATAAACA
36401 ACATTCAAAC CAGCAGGAC AAGATAAGAT CAAAGGCTT TTTCTGGAGT
36451 CAGAACTCT GTAATGGAAG GACCCCTGTT CTCAGTGGAG AGAGATGGAA
36501 CACAGCTTGG GAGGAATGG CTACCCAAAG GCGAGGAGG TGCGCAAT
36551 AGTGACAAG ATGGTGGACA CTTACTCAGT ACTTGCTATA TGCCAGGCAC

FIGURE 3L

36601 TCTAAGTGCT TTTCATGCAT AATCCACCTG GATTCCACC ACTGTTTGT
36651 GATGTCAGCC CTACTTTATC CCATTTTATA GATAAGAAA TTGAGGCTCA
36701 GAGAGGTTAA GTAACTACC AAAGGTACA CAGCTGGCAA GTGGTGAAC
36751 CAAGATACAG ACCCAGGGCA GGCAGTCCAG GGTATACAGA CAGTGGGCT
36801 GATTCCATCT CCTGTGGCT CCCAGACTCT CCTCCCCACT GTCTGCTACC
36851 TTCTGTGGC CTMTTGTGGC CAGCTGGTGT CACCAGCCTT CTGGCAGACA
36901 GCTCATCAGC CTGGAGGGTC AOCCTATGCC TGGCTAGAA CTGTTTGACA
36951 GCTCATATT CTGCCAGTC CTCTCTGCTC ACAGGTCCAG AGAGTGGACA
37001 CTGGGGAAAG GGTGGCAGCT AGGACCCAGT GAACCTGGTG AGGACCTGCT
37051 CAGTGAAGGC TTCAACCCCT TGGCAAAACC CTCTGTATGG TGGTCCCTGGT
37101 TTCTGTGCT GTGTCTGTCT GTCTCTGTGT CTCTGTGTGT AACGTGTGACA
37151 CTCTGCTTCT TGAGAACACT CAGGAGATGT CTTCATCTCT TGCACTTTGG
37201 CCATCCAGAG AACTTCCATG GCACCTAGGG ATGGAGCCCT CACTCTTTCA
37251 CCTGGGCACT CTGCTTCCAG GCCCTGGTGG AAGCTGTCAA AGGCAGAGTC
37301 CCAGTGGCC CAGGCGGCTC CAGTACTGAG CATGGTTTCT CCTCTAAGTG
37351 TCGTGCATCC ATGCCCTCTT CACGCGAGAG GAGATCTTGA GGTGCCACCC
37401 TGAGGGCTCT GAGGCCACTC AAGATCCCTT TCTTGTCTGAG AGGCTATAGG
37451 AAGTGCCTCT TTGCGGGTGT TCGGAGACC CTTCGCCCTT TTGTCAGACA
37501 CAGCACTCTC TTGTGGATCT GGTGCCCGA CTTCAGGTGT GGGAGAGGGT
37551 ACAATGCAGG AGACTTGATA TTCTCTTTTG TTTTCACAGC TGCCAAAAGC
37601 CTATTGAACA AGAAGTGGGA TGGCGGTGTC AAGGTAAGTG TCTCCAGCCT
37651 CTGAACAGAC TGGCTCTTTT CTCCCGCAG TCACCTATGG AATCTCTGGC
37701 ACCGTGTTCC CCTTTTCCCA GGGAACTTTC CTATCTTGC TAGTCTGCTT
37751 TAAACAGAT GCCTTTGTGC TCAGAACAGA AGGTCTGCTT GGCCTGAGAG
37801 GGAAGTAGGG AGGTATTTTT CCTGGCCCTA GCTGGATGGG AATGACTCAG
37851 GGAAGTGAT CCAATCATA GTTTATACCA GAGCTGAATC CGGAACCTGA
37901 CTCTACAGC GATGCTTCAT CTCCAGGCTT TGAATCTGGG TTTTITAGGT
37951 CATTTGGTGA TCTTCTTTT TTCTCTTTT AGAGCACAAA TCTTTTAAAT
38001 CAAATGAAAG CCAATTTTGC CTGAGTGATT CAGGCAGGGT ATAGGGCTTG
38051 GAACCTGAAA CCACTCTCTT TTGGTCTTT TTCTCTCTCT CTACAACT
38101 TTCAGATCC ACTGAGTGA ACAGCCTCGA GCTTCTTGA CGCATAGGCT
38151 CCTCAGAAA AGGCAAAAGC CATGGTGGAT CAGGCTTGT TCCACTGGG
38201 TGAGGGAGC TTTCCTATGG GACTGGGCA AGAGGAGGA CCTGGGACC
38251 ACCAGGAGC CTGCTGGGA TGGCTGCTTG GCGAAGGTAG AGGAGAGGTG
38301 ACTGGGGCTA CCCACAGGC CCAAGACATT CTGTAGATGC TTTGGGGCA
38351 GAAAGGATCC TGGGGCTAGG GCATTGGGA GGAGCTCATG CTATCTTGA
38401 GCTTCCAGC TTACACTCTA GACTAGATT TCACCTGGCC TTTTCCCAAG
38451 ATCTTGTGTC AACAGCTGAG ATACACACAC AAGCCCGGT CCTTCCCGT
38501 TCCCTCCCA CTCCCTCTC TTCTCTCTAT TCTCTGATG CCTGCTCTG
38551 TGTCTTCCG CCTCTGCGG GGGAGCCTGG GCTCCGCGCA CACCTCTGA
38601 CATGGAGCTG GGGCATCGT GCGTCCCA AGCTCTGCC CTGAGCTACA
38651 TGGATGAGC CAGGTGAGGA AAAGGGGAG GTTTAGTTGG AGAGAGTGT
38701 TAATAAGTAC CTGTGAGTCA GATGTCCAG CAGCAATCTG TTTCTAGGGG
38751 TACACAACAG AGGTGTAAGA GGGGGTGTG CTTCAGTGC CCATAGGAAG
38801 GGGGCGCAC CTGGAGTCAG CTGAGGCTG CTAGTGGACC CAGCGAGAT
38851 GGTITAGTCC AGGAAGCTCA TAGGAGAGAG GGTACTGAG AAAGCTGAG
38901 GGACATAGGT GAGACTCACT TTGCAGTTT ACTTTCTGCT ATATGTTTTC
38951 TTTAAATGA AAATATGGGT CAGGCTTGGT GGTCACTCC TGTAATCCA
39001 GCACTTTGGG AGGCTAAGGC GGGTGGATCA CCTGGGGTCA GGAATTTAAG
39051 ACCAGCCTGG CCAACCTGGT GAACTCCGT CTCTACAAA ATACAAAAT
39101 TAGCCAGTCA TAATGACCG TGGCTGTAA CTCCAGCCT CCGGAGTCTG
39151 AGGCAGGAGA ATGGCTTGAA CCTGGGAGC GGAGGTGCA GTGAGCCAAG
39201 ATTGGGCCAT TGCACTCCAG CCTGGGCGAC AGAGCAAGAC TCCGTCTGAA
39251 AATAAAGAAA AGAGAAAAGA AAACAACATG ACATTTCTAT AACTTAAAA
39301 CAACAATTA TATTGTATG GGTCTCTTA TACATATGA TGTCTCTGCT
39351 CCAGTGAGAA CACAGGCTGT GTGGTAGATT GATGCAAAA ATATGGTTGG
39401 ATCAGTCTTA TCAGGCAGAA TTGGAAGTT CTGTGTGAGA CCATGGGAAA
39451 TACCATAGGC CATTGAGCAG GGAAGCTATG GTGAGAGTGC TGATAGAAAT
39501 GATTTGGCAA GCGGGTGGG GTGGCTTAC TCTGTAAATC CCAGCATTTT
39551 GGTATGCTGA GCGAAGAGA TTGCTTGTAG CCAGGAGTTT GAGACAGCC
39601 TGGGCAAAAC CTGTCTGTG AAAAAAATA AAAAAATTA ACTGGGCATA

FIGURE 3M

39651 GIGGIGIGCA TCTGTAGTCA CAGCTACTTG GGAGGCTGAG GTAAGAGAAT
39701 TGCCCTAAGCC CAGGGAGTIT GAGCCIGAGG TGAGCCAGA TCAAGCCACT
39751 GCACCTCTCCA GCTGGGGTGA CAGTGAACC CTGCCCTAAA AAAAAAAAAA
39801 AGATACCTGC TGTGCCCCCTA GAAGTGTGGG AGGCAAACT TAATCTACCT
39851 TTTAAGGTGT TTACAGTGGG AGAGACACAA GGCAGCTACT GTTCTATGG
39901 AGTCTGTCTAA GGTCTCAGGG AGGTGTGCAC CTGGCAGGTG CTGGGGGAGC
39951 AGACAGATAA ACATCCAAAC CAGGACAGGA ATCTTCTTGA AGGAGATGGC
40001 CAGGAATTGA GCTTGAGGGA GTAGCTGGAT TTTGCTGGGT TAAGAGGAG
40051 ACAGGAGGGG AGGGATATTG CAGGCAGAGG GAAGAGGGCA TGTGAAGATA
40101 CACGAGGTGT AAACAGCATG ATGATTCCTG GAACCTCAGT ATCTCTTTA
40151 TGGCTGAAGG GAAGAGCAAT TGCATAAAAT GAGACCTGAA ATAAAGCAGT
40201 GACTGTGTAG GTGGAGGGGA GAGGATGGAA AAGGCACCAT TACAGAACAG
40251 GTTCTTAGCC AACCTTTCTA GATACTACTG GTGTCAAGA TGAAGGTGAT
40301 GTGCAGCCAT GTAAGATTAG CCCAAGGAGC CAGCTCAAAC CATGCACATC
40351 CAGGGGCCAG CTTGGAATTG ATGTTCTTGA GGCTTTGGCT GGGAGGCAGA
40401 ATCTGTGAAT TTTAAAAACA CTTTCATGAA TCCAAGCAC ATGAAGGTIT
40451 AAGAGTCTGG TAAAGGCAAA ATTTTGGGGT TATGTGTAA GAAAGGGCTG
40501 GAACAAGAGT CGGCAAGGA AACAGAGGAA GACAGAGAG GTAGGGGGAA
40551 AAGAGAAATG TGCAGCAGCT GCAGCTCTTC CAGGAACCTT CAGGATGAGG
40601 GCTGGGCAGA CACATCATTA GGTAAAGGCT TTAATGAGG ACGTGGCTGG
40651 GGAACCTAGC CCTGCAATGT GTTGTGTGTC TGACCTGAT ATGTGCTCAG
40701 TAAATGAGIT TTATGCCACA TTCTTTTGTG AAAAGAGCTT CAATATCATG
40751 GTGGGAACCA GAGGCCAATG ATCACCCTAA ATTAAGAGG CAACCGGTA
40801 TTGCGAGCGG TTGTGATGGG AGGGGTTAAT ATTTTATTTG AAAGAGTTTC
40851 TGTGACAAAT AATCCCTCTT AAAACCCAGT AGAAGCTGGG CGTGGTGGCT
40901 CAGCCCTGTA ATCCAGCAGC TTTGGGAGGC CGAGGCGGGT GGATCAGCAG
40951 GTGAGGAGAT CGAGACCATC CTGGCTAACA CGGTGAAACC CCATCTCTAC
41001 TGAAAAATCA AAAAATTAGC CGGGTGTGGT GGCAGGCGCC TGTAGTCCCA
41051 GCTACTTGGG AGGTGTAGGC AGGAGAATGG CGTGAACCGG GAGGCGGGAG
41101 CTTGCAGTGA GCTGAGATTG TGCCACTGCA CTCATCTCTG GGTGACAGAG
41151 CAAGACTCCG TCTCAAAAAA AAAAAAAAAA AAAAAAAAAA ACCAGTAGA
41201 TAGGCTAGGT GTGGTGGCTC ACATCTGTAA TCCAGCACT TTGGGATGCT
41251 GAGGTGGGCT GATCCTTGA GGCAGGAGT TCGAGACCAG CCTGGCCAAC
41301 ATGTGTGAAC CCCCTCTCTA CTAAAAATAC AAAAGTATAG CAGTAGTGGT
41351 GGTGCACGCC TGTAGTCCCA GCTACTGGG AGGCTGAGAT AGGAGAATCA
41401 CTTGAACCTT GCGGGGGGCA GAGGTGTGGG TGAGCTGGGA TTACCCACT
41451 GCACCTCCAGC CTGGGGGACA GAGCAAGACT CTGTCTCAA AAAAAAAAAA
41501 AGGAAGATAG ATGATCAAG AAAATAACT GACAACCTGA AAACAAGGAA
41551 GTAGACTTGG ATAACAAATG TGGAAAAAT TCTAGCCTCA CTAGTATCAG
41601 AGAAATGCAA ATTGAAACAA GGTGCCATTT TTGACTCTTA GTTAGTGTG
41651 GTAGTGAATA CCAGATGGT CCTTTCTAAA ACAGCCTGTG TGTCAAAACC
41701 ATAAAAATGC TTCTACCTCT TTTTACCTG TTAATTTCTAC TTCTGAGAGT
41751 TTTTCTTAAA GAAATAATTC AAAATAGGAA AAAGCTAAAA GCAGAAAAAT
41801 GTTGAACATG ACATTATTTA TAGCTGTGGA AAGATTGGAG GCTGGGCACA
41851 GTGGCTTATG CTTGTAACTT CAGCACTTTG TGAGGCCAAG TTGGGAGGAT
41901 TGCTTGAACC CAAGAGCTTG AGACCGCCT GGGAAACGTA GTGAGACCC
41951 ATCTCTTAAA AAAAAAAAAA AAAATTAGCT GAGTGTGGTG GAACGTGCT
42001 GTAGTCCAG CTACTTGGGA GGTGAGGTG GAGGATTGC TTGAGCCAG
42051 GAGGCTGAGG TTACAGCCAG GATCACCA CACTGCTCCA GCTGGGTGA
42101 CAGAGTGAGG CTCTGTTTAA AAAAAAAAAA AAAAGAGAGA GAAGAAAAA
42151 AAGATTGGAG ACAATTTGAA AAGCCAGTAA GGAGCCAGAC ACAGTGGTGC
42201 GTACCTATAG TCCAGCTAC TCAGGAGGCT GTGCGAGGAC AGAATTGCTT
42251 GAGCCAGGA ATTGAGGCC AGCTGGGCAA CATAGTGAGA CCCCCAATC
42301 TTAATAATGT TTTTAAATTT AAAAATAAAA AGATTTTTTA AAAGCCAGTA
42351 AATGACTAAA TAATATGGG AATCTTACTT AATAAATAT TCAAAAGTTA
42401 TTAATTTTCA TGACCGTAGG GATATTTTAA GTGAAAAATA AAGTGCAGAA
42451 ATGTTTATA TTAAGTGAAG GAAGTGGTAT ATAAAGGAGT ACAGACAAGC
42501 CAGGACCGGT GGCTCAGGCC TGTAAATCCA GCACCTTGGG AGCCCGAGGC
42551 AGACAGATCA CGAGGTCAGG AGATCGAGAC CAGCCTGGCC AACATGGTGA
42601 AACCCGCTCT TTAATAAAA TACAAAAAT AGCTGGCGGT GGTGGTGGT
42651 GCTGTGAATC CCAGCCACTT GGAAGGCTGA GGCAGAGAA TCGTTTGAAC

FIGURE 3N

42701 TAGGGAGTGG GAGGTGGGG TGAGCCAAGT GCGCCACTGC ACTCCAGCCT
42751 GGTGACAGAG CAAGATTCTG TCTCAAAAA TAAAAAATAA AAGGAGTACA
42801 TACACTATCA TTCTAAATTT GGTTCGAGA AACGGTTTG TAGATATTTA
42851 TTCTAGTATAT AATATGTGGA TAAAAAAGGG ACTGGAAGAA AGCCACTAA
42901 GTGTCAACAG TAACCTCACC AGGTGATGG AATTGAGAA ACTTTTTCG
42951 TTACACATTT TCTGTATTC CTATATTTT CATCTAGATT GTGCACTACT
43001 GTTATCAGAA TTTTITTTAA ATACTATTT TTTTITAAAG TAAAGCATAA
43051 TACCAGGTGT GCAACTCAT GCGTGTAAAT CCCAGCTACT GGGAGGCTGA
43101 GGTGGGAGGA TTGCTTGAGC CCAGGAGGT CAGCCTGGGC AACATAAGCA
43151 AGACTCCATC TCAATTAAAA AAAAAGAAA AGAGGTAAGA CATGTGCTTG
43201 TATTTATATA TCTTATAATG ATATCTTTT TTTTGTTTT TGAGACAGGG
43251 TCTCACTCTG TCCCTTGGC TGGAGGTAG TGGTGTATC TTGGCTCACT
43301 GCAACCTCCG CCTCCCGGC TCAAGTGAAT CTTCCACTTC AGCCTCCIGA
43351 GTAGCTGGGA ATACGGGCAT GTGCCACCAC GCGCGCTGA TTTTGTATTT
43401 TTTAGTAGAG ACGGGTTCG CCAGGCTAGT CTGCACTCC TGAGCTCAGG
43451 TGATCTGCCC GCTCAACCT CCTGAAGTC GGGGGTTACA GGCATGAGCC
43501 ACCAGGCTTG GCTATAATG ATATCTTAA AGATTGCTTT CTTTITTTT
43551 TTTTITTTT TTTTITAGAC GGAGTCTAC TCTCACCAG GCTGGAGTGC
43601 AATGGCATGG TCTGGCTCA CTGCAACTTC GCGCTCCGG GTTCAACAA
43651 TTCTCCAACC TCAGCCTCC AAGTAGCTGG GACTACAGGC GCGTCCACC
43701 ACACCCAGCT AATTTTATA TTTTITAGT AGACGGGGT TTGCTATGTT
43751 GCGCAGGCTG GTCTGATCT CCTGACCTTG TGATCCACC GCTCAGCCT
43801 CCCAAGTGC TGGGATTACA GGCATGAACC ACCGTCGCC GCAATTGCA
43851 TTTTITAAAA AGACTGGAAG ATTGCTAGGA GTATTAGTGG TTTTCCCATG
43901 CCGCTTCTCT GTTTTCCAA TTGCTGTAT TGTGGCTGCA GTCTTTTAT
43951 AATATGAAC AGGTAAATAA CAACCTATGT TGTGGCTGCA TCAAGGGGT
44001 GAGAAACGAA AAGGAGAGGA CAAAGCAAGA TGTGAGAGT TCGACCTTTC
44051 CAGGCTCTCT CAAAGTCAAG GTTTTGATCA ATGTTATGAG GGAGGCTGT
44101 GAGTAGCTC AGATGGCTT GAGCTTTCAG CATCATGGAT TCTTCTTTA
44151 GATCCCATCT TCCCTTCCA ACTCCCTCT CCTCAATTC TACTGCTTAA
44201 GTGTCCATAG GCGATTCTT TTTTCACTGT TCAGAAGCTT TCTGCAAGAT
44251 GTTCAAAATA CTAGCATTGG TTTGAGCAGC TAGTCTGTCT TGTTTCTTG
44301 ATTTGGGGGA CTTAGCTTCT ATTTAGATT CTTTGAAGCT GGATGCCAGT
44351 GACCCAGGCT CTATGGAAGA GTAAGAGCCA CTTGTGAGGA TGACTGAAGA
44401 GGCACAAC TCTCAGATCC TGAGAGTGTA GGACAACITG TGCTTCTGC
44451 TAGTCCAGG CCAGATGGC CATCTTATCT TAAAAAAGA AAGCAAGCAA
44501 GAAAAACGAA AGGTATATGT TATTTCCCTA AGTACTATTT GAATATTTT
44551 GTTAAATTA GTATGAGAAA GAGGTITGAA GCTTTTCCA GCTTAAATTT
44601 TAAATAAAT ATACAGTTT TAAGTAAAAG TGAGATATGA TTCTTTAGAA
44651 ATCATCTGGC ATTTAGCCAG GCATGGTGT GTGCCCTGT AGTCTAGCT
44701 ACTCAGGTG CTGAGGAGG AAGATCCCT GAGCCACGGA GGTGTAGGCT
44751 GCAGTGAAC ATGATCATGC CAGTACTTCA GCGCGGCAA TAGAGCAAGA
44801 CCTTATCTCT AAAAAAATA TAAAAAGAC TCACATTTAG ACAATGTGT
44851 AGTGTGCTGG TTGAGAAGGA GCGCAGCTAT GCATGGCTAA GGCATAATCC
44901 CTGAATGGAG AAGGAAATG AAAAATGTG ACTAACCTGA GAACAGTCT
44951 TTGAAAAGG GTGATCTCAG GTTCTCATGC AGGCAATTT AGGAAAAGA
45001 GAGCAAGCCA GGAGAAGGCT GAGAATTTAT TCCCAATTAG TCAAAAATCT
45051 GCTTTAAGTC AAGATCTGC AATGGCTTT CACAACAAGC CCGTAAAAAT
45101 CAGCAGAACA AAGACTGGGC CTGGTGTGAG AGTGCTTACG CAGAGTCTTT
45151 GCTGCGGTGA TTGAGTCAA GTTAGAAAC TGTGCTCTTC TTGAGCTGG
45201 GAAAAACCA AAGTCAGCA ACCAGCTCA ACTCAGCAA CTTGTGTGC
45251 CTGTATGCTA ACTATAAGG ATGTGTCTAG GTACTGTGGA AATTGTAAAG
45301 ACACATAGA TAGGAACCTT CCGTAAAGCA GTAAACATTT AGTTGGGTAA
45351 AGGGATAAGG AGATATACAC ACACACACAC ACACACACAC ACACACACAC
45401 CCCACTACTT ATATATATGA ATATAAGGA ACTCCTTCTT TTTGAGGGAT
45451 CATTTTCCAA GTAAAAATC ATATTGAGC ATATTAAAA GGCACATGTA
45501 AGGCTGTGTG CGGTGGCTCA CGCTGTAAAT CCCAGCACTT TGGGAGGCGG
45551 AGGTAGGTGG ATCACTGAG GTAGGAATT CGAGACCAGC CTGGCCAACA
45601 TGGGAAACC AGTCTCTCTA CTAAAAATAC AAAAAAATC CAGTGGGGCG
45651 TGGTGGCGG CGCTGTAAAT CCCAGCCTT CAGGAGGCTA AGGCAGGAGA
45701 ATGTCTTGAA CCAGGGAGGC GGAGGTGCA GTGAGCCAG ATGTGCTCAC

FIGURE 30

45751 TGCACCTCAG CCTGGGCAAC AGAGTGAGAC TOOCTAAAA TAAATAAATA
45801 AATAAATAAA TAAATAAATA AATAAATAAA TAAAAGGCA ATGTAAAAGA
45851 GGCTAACTA TATTTAGGTT TTCTTTTTC TTTAAATCTA ATTCTAAATT
45901 ATGACCAATT GTCAATATTT GTAGCTCTTT TGGTGTATTA TAATAATAT
45951 CCTGAAAAT GCTTCTTAAA GAATGCTGGC CGCTTGAGGG CAGGAGCAGT
46001 TTATCAGCTG TGTTTACCTG AAACAGCCCT CAGTGTTTGC TGGGCATTGT
46051 TAAATGAATG TGCAAAAGTT GAACGACAGA CGACATATT ACAGGGGGAC
46101 CTTACCCCA GTGAGCTAAT GATGACATTG ATAATTACCC TTCATTTTTT
46151 AGACACAGTC TTCTGGGATA TATTTTCAGT GTTCCAGTG GTCTTCATCT
46201 TGATGGTCT GTTTCACATG TGAACGTAAA GTTGGTGGC ATCTAGTTGA
46251 GGCTGAGGAA TCACCTGCTTT CAACATTCCT TGTTGGCTTAC ATCCCTGCAT
46301 TTTTATGATC ACTGTAGTTT TAATCACTGG CACTCTGTG TTCTTAATTT
46351 CCACGAATG CAAAATGCAA TAAAAATTC AAATATTGTA AACAGCATG
46401 GCTATACCTA CAAAGGAAG CCAACATTTA ACTGCTAGGT GATTTTCAAA
46451 AGCTCAGCAT CTTTATGTAA AAAGCATAGT AGGGATGCG CAGAGTCAGA
46501 AGTCAAAATT TATTAGAGCT GAGGAGAGCC TGTAGTAGCT TTGCTTTTT
46551 CCTGGTGGC TGCCTACTTG AATTTTCAGC AGTTCTAGTA ATGAGAGAAA
46601 ATAAATAACA TTACAGGGTG AGCTAACCT ATGAACCCAG ACCTGTAAT
46651 TGTAGCAAA ATGATACTTA ACCTCACAGA CTGTGTCTT AATCTCCTTA
46701 AGAGGCTTTT TTTGAGCAAG GCTGAGACAT CTCAGAAGAT ACTAAATCTG
46751 TGTCTATGAA CCTGACACA AAAGAGTTCT TCCCTCCAG GGTCTGGAGG
46801 GTGTAGTGC CTGTGGTCT GTGTGCTGTT TAACCTCTG GTGCTGGACT
46851 CGGGGTCTCC CTCCGCTCTT TTCTCCCTGA TGCAGAGCC ACACGTGGTC
46901 GCTAACCTGC AGGCTCTCTG TGCTTCTCTT CTACCTCTT CTTTCCCTT
46951 CTCCTTCCCT CTGTCTGTGG TGTGTCCAGA AAAGGAGTC GAGTTCCAGC
47001 GGTACCTTAA TGGTGAAGCT TGCTGCCCCA CCAATGCCC ACTCCATGCT
47051 GCTGTGCCC GCTGCCCAGC CAGGCAAAAC TGTCTGCGA CGTGGGTGTG
47101 CCTCACTCAT CCTCACTGCA TGTCTGTGCT GTGTGGGCG GTGTGGCCIG
47151 TCTTGGCAGG CGGGGGCCAT TGCCCAAGGT CACCCAGTAG CCTAAAAAGT
47201 GGACATTGGA AGGGGTGGTA CGGCACCCC TGCTGTGGAG CTGGACAGA
47251 CCCCAGGCAC CCAGGGTAGG ATGTGAAGCT GTTAGGGACT TGGGCAAGC
47301 AAGGGAGAGA CCCCACCTCT CTGTGACCC AGAAGGAGAG GCTCTGCTTC
47351 CCAGGCATGA GGAGCTGCTT CCTACAGACT GGCAGCTGA GGGCAACTGT
47401 GTGGTGGGCA GAGGAGCTGG TTGCAGGCTC CCACTGTGA GTCTGCTCT
47451 CCTGGCTCTG CCCCCTGCA AATCCCATTC TCTCTAGCTG TGCCAGTGG
47501 TTTATTTCTG CCACCCAGCC CTGGGGGAC AGCTAACTCA TCTTCTCAC
47551 GGGACACTGG GCACCAAGGG CAACACAGCA GCTGAGTCA TTATGAAACC
47601 ATCCATTAAA ACCAGAGGTG GGGGCCGGGC GCATGGCTC AGCCCTGTAA
47651 TCTAGCACT TTGGGAGGCC GAGGCGGGTG GATCACAAG TCAGGAGATC
47701 AAGACATAA CACGGTGAAG CCTGTCTCT ACTAAAAATG CAAAAATTA
47751 GCGAGGTGTG GTGGTGGGG CCTGTAGTCC CAGCTACTCA GGAGGCTGAG
47801 GCAGGAGAT GGGGTGAACC CAGGAGGCG AGCTTGCAGT GAGCCGAGAT
47851 CGGCCACTG CGCTCCAGCC TGGGCGACAG AGCTAGACTC CGTCTCAAAA
47901 AATAAATAAA CCAGAGGTGG GGCACCTTGG GTGACATCCC AGCCCTCTGC
47951 AGGTTTGTG GGCACCCTGG AGTCCCTGCC CCTGTGAGG GTCTTGGCT
48001 CAGCTGGGAT TTACAGGTAG GGCAGCCCTC TCTAACCAAC CCGAACAGG
48051 TCAGCATCAT TCACCTAGCT AGGTGGGCTT TGCTTCTTGG TGGGAATGAG
48101 AGACAGCAGA GCTCCCTGTA GTTTAGACCC ACGTCTCAC TACTCTGGG
48151 CCCCCTCTTC TCTAGCCTGT CGCAGTCTGT GGAGTCTTGT TCAGTGGAGT
48201 CACTTGGTGC CTGGCTTGG GTTCCATGCC TAGCCCTGGG TTTGGGGATG
48251 TCTGAGCAT TGACAGCAAG CTGGGGTGG ACGGCTCAG GTCTGGTCCA
48301 AGAGGCTCC AGGCAAGAAG TAGGACAGTC AGGATGCTTT CTGTGTATGT
48351 CTTAGGAGAG AAGACACACA TTCTAGCTGT CGATGTATCA TCTGTGCCCT
48401 GTGAGGAGT GGTAGCCACA CATTTGTCTC ACTGCCATTT GAAGAACTTG
48451 CAGGCATCAG GCTGCTCTC AGTGGCCCC AACCCACTG GAACCTAGTG
48501 AGATGGAGTA CGCTGGTTAG GGAACATCA GAGGCAAGA ACATCACATG
48551 GATATGGCTC CTGCCCCTGG AGATCAGCCT TCTTCTTTC TTCCATCTTC
48601 CCTTGGCCC TCCCTTGTG TGCCCCCTCG TGTAAATGTT TTGTTTGTTC
48651 GTTGTCTTTT GTTTTCTTGA GATGGAGTCT TGCTCTGTG CCGAGCTGG
48701 AGTGCAGTGG TGCAATCTTG GCTCACTGCA ATCTCTGCC CCGAGTTCA
48751 AGCAATCTC TTGTCTCAGC CTCCCGAGTA GCTGGGATTA CAGGCATGTG

FIGURE 3P

48801 CCACCATGCC CGGCTAATTT TTGTATTTT AGTACAGACG GGGTTTCACC
48851 ATGTGTGGCA GGCIGGTCTT GAACTOCTGA CCTCAGGTGA TOCAOCCGCC
48901 TTGGCCTOCC AAGTGTCTGA GATTACAGGT GTGAGCCACC GTGCCCACCC
48951 ACCCAACATG TAGTTTGTGA AGGCAAGGAG ATATOCCCTG TGGTCATGGT
49001 GCTGTGTGGA ATGTGTGGCT GTGTGTGGCC TACTCTGTCC TGGGGGCTGG
49051 ATTCTGGGAC TACAGCTACA GCGCCGCTGG GTTTCACCTG CCGCTCCCGG
49101 GAACACTGCC CTCTAGCTG ATCAGGCTTA AGATTGTGCA GACAAAAGG
49151 TGAACAGCAC AGTCTGACT CTGCTOCTG AGGTACGTGA ATGCATTTTG
49201 TGTCTGAAG GGACTTCCAC CCGCATCTC TGGACACCAT CTCTAGGCC
49251 AGGCATACTT TTCTTTTCTC CTCTCTCTTT GTTTCAGGCT TGGAGCTGGT
49301 GTTGTAAAGG GGAATATACG GTGCTGGGT GAAAGTGCAG CAGGAGACTG
49351 CCCACAGATA GGGGACCAGA GTTCTGAAT TTTGTTCGTC TTCTTTATAA
49401 ACTACCCCCC TTTTCTCTGT ACAGTGGGAA GAAGATCTTG AACTTCTTTG
49451 GGTGAGGTGT GGATTTTGA ATGACCTGGC ACGTGGCATA AGCAGAGATT
49501 TCTGGAGGGA TGCTTTAAAA CAAGGCTTTG GCGTGGTCCC ACCTTGAGGG
49551 TGCCCCCACA GCTAGGTCTC TGGCCCCAC AAATACCTCC TCTGATCATC
49601 TCTCTAGCCA TCGCTOCCAT CTACACAGCG TTATGGAGGC CACCTCAGGC
49651 CTACCTCTC CAGGCCAGAC CAGGGGCAA GGGAGTCTG GGAGTTGAAC
49701 CTGAGTGGCC TTGGGGACTC TGGAGGAACT AAACCATCTG TTTTCTTGTG
49751 TCAGCCACAG AGCAACAACA AAAACAGTCT CGTAAGCCCA GCGCAAGAGC
49801 CCGGCGCCCT GCAGACGGCC ATGGTACCTC CTGACTACAG CTCTCCGCC
49851 TCTGACCTCT GCTGCCCTCT GCGCCCTOCC TCTTCTCTCT CTGTGCCCC
49901 CTCTCTGGCC TCGTGGCTGT TTCTTTCTCT GGTCCCATTA GAACGTACTG
49951 CTTTGTGTGC CGCCCTGTAT GCGCCCTOCC CTCTATGTG CCGCTGGCC
50001 GCGCTCCATC CCGCATGGCA GAAGTGTCTC TCGTCTCTCT GCTCTTTTGG
50051 CTGTGTGGGG GAAGAGTGT CAGGGCTCTC AGCTGAACCT CCGAGGCCCA
50101 GCGCAGGACC CCTAGTGGGT CTGCTGTGGG GCGTGGGAAG GTGAGTTGCT
50151 TAGGAAAGGA GAGGGTAGGA GCTTTCTTGG GACCTGAACA TCAGTTCTTG
50201 CAGGCCCCCT GTTAAAACTT GCGTACGCT CTCTCTTGA AAGCCAGAAA
50251 CAGGAAAGAG GCGTGGGGTC CCGACCTCTG GATGGTGTG AGGTCTCCAG
50301 GCTCTGGAG TGGCTCATGC TGGCTAAGTT CTCTCTGGGC TCTCCAGGG
50351 GTTCTGTGTG CTCTTGGAGG TCGCTCTGCT AGTGGTGGCT AACTAGAGAG
50401 TCAGCAGGGG GGTGACTGGG AAAGAGGGAG AGGTGATGTT GCGTCTACT
50451 CCGCTCTCTG CCGACCTCTA TACCAGTGA CGTGGCGGG TGGGCCAGG
50501 AACTAGGGAA GGCAGAGGC GCGCGAGTG GCGAGCTCTC TGGGCTCAGC
50551 TTGCTGAGGG GCGCTCTGT CCGGCTCTT TCTGGGAGAC CTCTCTCTC
50601 TGCCCATGTT CCGCTCTAC ACATTCOCC TGATGAAGC TGTGGCGGG
50651 GCGCGCGCTG TGGCTCAGT CCGACAGCTC CTCTAGTGA CCGCGCCGT
50701 GGGAACTCCA TGTGAAAGA GCGCTCAGAA CTGACAGGAA TCAGGACAG
50751 AGGCGCTTGC TGTACGCTC CTGGCACCT GCACTGCA GCGCTCTCT
50801 TCTTACAGC CCGTGTCTG TCGCAAAATC CAGGCTATC CCGCTGCGC
50851 GGGACCCAG TTGAGCGGG ATATTTTGTC TTCTGGAGAT GCGTGGTGG
50901 CAGGCTCAG TGGTATCAT AGGGTCTGG GGGTCTCTG GGTGAGGTG
50951 GGGCTCTCTA GGGAGAGCC ATAGTCTGTC CCGAGTGGG AAGGGTAAATC
51001 TCTATCTCT CTACAGGAG CCGCAAACTA CTGTGGTACA CAACGTACA
51051 GATGGGATCA AGGTGAGTGG CTCTGAGCC TGGCTCTGCT TTTCCAGGT
51101 AGCAGGAGAC AGGTGGGCTG GGTCCAGGG GTCTACAGGC TGCACCTGA
51151 GCGCAAGGTG TTTGCAAGG CTGAGCTGAA GGTAGCTGT GCGCAGGTT
51201 GCTCCATGCT GAGGAAGGG ATTTATACCT ACAGAGCTCA GCGTTTGCAG
51251 TCAGACAGAC CTGGTCTGAA TCGTGGCGCT GCACTTAGT ATCTTTATC
51301 TGCAAAATGG GGATGATAAT AATAGAATCT TCTCCATAT GTCCGAAGTT
51351 TAAATGAGAG TAAAGTTTCA CTGAAAAAT AGGCAAGAGT ATCTCCAGAC
51401 CCGTGGAGGT TCTCCATGGC CTGACCGCT TGTGCGCTG ATGTCTTAC
51451 CAGCATCTCT GAACATCTGT TAAGCCAGG TAACATCCAT GCGTCTGGCT
51501 TACAGAGGTG ACAAGACAAA TTATCTGTTC AAACGGTGG TGGATGGGA
51551 GCGAGATAAA AAACCAATAA GCAACAGAT AAGATAAGCT GCGCACCGTG
51601 GCTCACACT GTATCTCTCA CACTTGGGA GCGCAAGGTG CCGAGATCGC
51651 CTGAGCTCAG GAGTTAGAGA CCGCTTGGG CAACATGGTG AAACCTGTG
51701 TCTACTAAAA TACAAAAAG TAGGCAAGGT TGGTGGCGG TCGCTGTAGT
51751 CCGAGCTACT TGGGAGGCTG AGGCACGATA ATTGCTTGA CCGGGAGGT
51801 GGAGGTGCA GTGAGCTGAG ATCAGGCCAC TGCCTCCAG CTGGGCTAC

FIGURE 3Q

51851 GCAGTGGAC TTAATCTCTC AAAAAAATA AATAAGATAA AATCTAATGT
51901 CAATAGGTAA TCTGAAGAAA ATGGCAGAAA GTAGAGAGAG GGCCAGGTGC
51951 GGTGGCTCAT GCTGTATATC CTAGCACTTT GGGAGGCCAA GGCCGGCGGA
52001 TCACCTTGAGG TCAGGAGTTC AAAACCAAGC TGGCCACAT GGC AAAAACC
52051 CATCTCTACT AAAGATACAG AAATTACCTG GGGATGGTGG CACATGCCCTG
52101 TAATCCAGC TACCTGGGAG GCTGAGGCAG GAGAATGCTT TGAACCTGGG
52151 AGGCGGAGGT TGCAGTGAAC TGAATGCTG CCACTGCCTT TCAGCTGGG
52201 CGACAGAGCA AGACTCCATC TAAAAAATGA AAAACAGAAA AACCTCAACA
52251 AACTAGACAG AGAGAACAGG GCTTGAATT AAGTAGTCAG GAGAGGGCTT
52301 CTTTCAGGAG GTGATATCTG AGCTAGAAAC TGAATGGTGG GTGGGAAGGA
52351 GGCAGCCAGG CCAGCTCTGA GCTGAGTGC CCTAAGCAGA AGGAACAGAA
52401 GCTCAGATGT GGCTTTGTGA ATCAAGCAGA GGGAGAGCA AAGTGAAGG
52451 GGGAGAACCA TAGGAGAGTG ATGAGGTGG AGAAGCAGCA GGGCTGCTA
52501 CAGAGGCCCT TGATAGGAGT TGCACTTTCT TCCAGCAGA AGGAGAAGCT
52551 ATTGGGAGTT CTTAGCAGGA GTAACAGAA CTAGTTGACA CTTTAAACA
52601 CCACCTGGC CTCTATGATC AGAATCTAG GAGGCCCCG GGTGGTGGC
52651 TCAGGCCGT AATCCCTGCA CTTTGAAGG CCGAGGCCAG TGGATCAGCA
52701 AAGGTCAGGA GCTCAGAAC AGCTGGCCA ACATGATGAA ACCCATCTC
52751 TAATAAAAT ACAAAAATTA GCCAGGCATG GTGGCAGCA CTTGTAATCC
52801 CAGCTACTCA GAGGCTGAG ACAGGAGAT CACTTGAAAC CCGAGGCCAG
52851 AGGTGCACT GAGCCAGAT CATGCCATG CACTCCAGC TGTGCAACAA
52901 GAGCAAAAT CTGTTTCAA AAAGAAAAC TCTAGGGAG AGGTAGTGT
52951 GGAAGTTAGG GAGACCATGA AGCTGTATC ATGGTTTCCG TGTGAGATGC
53001 TGGTGGCTG GAGTCAGGT GTAGCTGTGC ATTGGAAGT AAGAGGTAG
53051 ACATGGGCTT TACTTTGGAG GCAGAACAG AAGATTTTAT TTTAGATTGG
53101 CGCATCTGAA TATTAAGGGA AAAGAGAAAG AGAAGGATTG AGGATGACTC
53151 CAGGTTTTCG CTTGAGTAAC TGGGTAGATG GTGGCATTTA CCACTGGGG
53201 GAAGACTAGG GAGGGGATTT GGAAGAGTC AGACAGCCAG GGTGAAGCA
53251 GAACCTTCCA CAATTCCTCC TTGCACTCT TGTAGGAGCA GAACTCTGC
53301 TTTTGTCTG CTTTGTCTCT CTGGCTTCCA AGGGATGGAG CATATAGAAA
53351 CATGTTCTTT TTGGCTTACA GGGCTCCACA GAGAGCTGCA ACACCAACC
53401 AGAAGATGAG GACCTCAAAG GTAGGTGCTG GCGCTTGGAG GGGGAGGAC
53451 TCCAGCAGTG ACCCAGGTAC CTGGGCTCCA ATGGGGCACC TGCTTTTCT
53501 GTCCCCAGAA CTGGGAATGC TGGCTCTTAT GCGCTAGGA GAGGCTTGG
53551 TATAAAGCT ACCTTCCACG AGCCAAGATA TGAGGCCCT GTCTGGTGT
53601 GCTGAGTTGG GCAAGAGGCT TCTCTCTTT GACCCCAAGT CTAANAATAGC
53651 TAAGCTAGAG ATTCTCCAGG GCGCAGGCT CAGAGACTG TTCTGTGTC
53701 TGATAATGAT GTGCCATCCA AGAACAGGGG TACCCCAAGT CCGTCCCGAA
53751 GTAGCTGTGA AGTGTCTATG GTCATAAATA GAGTGACCAA TCACTCTGTG
53801 TTTTCTCTG ACACAGAACT TTTGGTTTGA AGACTGTGAT GGGCCAGGAG
53851 TGCTGGCTCA CACCTGTAAT ACCCAGAACT TTGGGAGGCG CAGGCGAGAA
53901 GGATTGCTTG AGACAGGAG TTTGAGACAA GCTTGGGCAA CATAGCAAGA
53951 CCTGTCTCT ATTAATAAATA AAAAATAGG AACAAATATA TAGGCCAGGT
54001 GCGGTGACCT ACACCTGTAA TCCCAACAT TTGGGAGGCC GAGGCAAGTG
54051 GATCACTTGA GGTCAAGAGT TCAAAACAG CTTGGCCAAC ATGATGAAC
54101 CCGTCTCTA CTAATAATAC AAAAAAGGC CCGGCTAGT GCTCAAGCC
54151 TGTAATCCA ACACCTTGGG AGGCCAAGGT GGTGGATCA CTTGAAGTC
54201 AGAAGTTCAA GACCAAGCTG GCAACATGG TGAACCTCCA TCTCTACTAA
54251 AAATATAAAA AATTAGCCAG GTGTGGGCA GTGGCTGTA ATCTAGCTA
54301 CTGGGAGGC GGAGGTGGGA GAATGCTTG AACCTGGGAG GTGGAGGTG
54351 CAGTACCGG AGATCACCCC ATTGCACTCC AGCTGGGCA ACAAGAGCA
54401 AACCTCTCT CAAAAAATA AAAAAAATA AAAAAATTAG CCGGTGTGG
54451 TGGCGGGTCT CTTGTAATCC AGCTACTCGG GAGACTGAG CATGAAATG
54501 GCTTGAACCC GGGAGGTGGA GGTGCACTG AGCTGAGAT GCACTACTGC
54551 ACTCCAGCT GGTGACAGA GCGACTCT GTCTCAAGAA AAAAAAATA
54601 AAAAATATAT ATATATATAT ATATATATAT ATATATATAA ATATAAACC
54651 CAGATAGTCC TGGGAACACT GGGATGAGT GTTCACTCTA GTCTTAAGAT
54701 TTTGGCTTGA ATGATGGAGT TGGAACTAAT CTGACACCG TGAGGCCACA
54751 TTTGGTCTAG TCCGTGGTGG CCGTGAAGG CCACTAGCTT AAGCTTGGC
54801 CTGGCTAGAG TGCCAGGCG GTGGAGGCG ATGGCAGGCT GGCACCCCG
54851 GAATCTCTGT CCGTCTCTT GATTGGGCT CTTGGAATTG CTTCTTTC

FIGURE 3R

54901 CTGAATTCAG TAAGTACCT TGGGCCAGGA CATCAGAAA GACAGAGGAA
54951 CACTCTAGGA CAGAGCTGG AGAGCATGCC CTGGGTTGCA AGGGGGCACC
55001 AAACCTTTTG GAACCAAAA AAATAGCAGA AAGCTGGGAG GAAGTGAATC
55051 ATAGTAGCTC CAGGCCCCTG TGAGTGAAGT CAGATCAGTT TTGATTCCGG
55101 CACTGTGGC AACATAGGAG GGGCTGTAC TGCTGGGCTC TGGACCTGT
55151 GGGCTGGGCC CTGGGAACAT CTTCCTGGG ATCAGGGGTC CTGGACAGG
55201 CTGTGTAAAG GCTGTCTGG AAGCCACAGC CCAGGTCTGG GCACCTGGCT
55251 GGTGCCCCA GCTGGGAGGC CTCCTGGCA GAGGGGGGG GGTGGGATGT
55301 GTTCCAGTGT CCACAGCAGC CTGAGGGAG GGGTCCCCCT GGGGGGCTC
55351 TACAGCGCCA TGGGCTGGG GCTGTCTGG CTGTCTGGT CACTGGCTT
55401 GTTCTGTTTG TTTTGGCTGC TCTGCTTGC CTTGGCTGC CTTGGCTGG
55451 CTGGCTAGCT GGGGGCTCC GCACTGGGA TGGCAGCTG GTGGCTGAAG
55501 GAGGGAGCTC CCGGACAGA ACAGCCCCCT CTGCAGGCAT GCAGCCCCAG
55551 CCTCTCTCT GCTCTCAGC CAGTAAAGT GAGGGAGGCA CATCTGGCT
55601 TGGTCTTCC TGGCTGTTC TGAAGCCCC CAGGGACCC CACCACAGCT
55651 GTAGTCCA CCACCTGCC CGTGGTAGTA AGCTCTGGG GCAITGGCTC
55701 TGCTGGGGGT GGGGGGTAGA CTGGAGGTG TGTGTAGAC AGGCAGGGC
55751 CCTGAGTCT GGGGCCAAA GAAATATGAG AAGTGTGGT GGAATAACAT
55801 GGGCTGGGAT GAGGGGAGTA GAAAGCCCC AGGATGTGA GTGGGCTTG
55851 CCTCAGGCT GAGCCAGGA GAAGGGCAGA GTGGGAAGTC AGGTCTGGG
55901 GGGTGGGAGT GGGATGATG GGAATCTGT ACAGCGAGGA ACTGTGTGG
55951 GGAATGAGT CTCTCTGAG CTCAGCATA CAGTATTAG AGCATGGGT
56001 CAGAGGCAAG ATAGATCTGA GTTAAATCC CAGCTACACT GGCCTCAAGA
56051 GTGTGAAGTT TAACCTCCA GAGCTGCAG TTCTTATCT GTAATGTGA
56101 AATAAATGG CAGCCACTC AGAGCCTTGT TAGATAAAG ACAAGGCAGT
56151 AGGAGTCTT GATACGGTG CTGATGGGT TATCAGTAGC TCATCTCAT
56201 ATTCTAGTT ACGTCTGTG TGGAGGATG CTTGTCTGC TGCTTTTCT
56251 CCAACATCT ATCTTGCAG AGTTCTAAG CACAACCTC TTGGGGGTG
56301 GGGCCCCAGT CAGGTATCC AGATGGGTCT GGTGGGGTGG GAGAGGGGT
56351 GTGTGTGTG GTTGCACAC TGCTGTCTG TTTTGAAGC CGATGAACT
56401 CCTGTCTTC CTAAACCTG TGCTGTCTA CCTGGAGCTG TGGCTAGCG
56451 GGGCTAGCG CTGTGGGGC CCTCTGGA TGTTGCTTTG GCTGGCTGC
56501 CCTGTCCAA CTGTCTGCT TGGCTGTCT GGGGGGGCTG GGGGTGGTG
56551 GTGTGTCTT AAGCTTGA GGTGTCTGC AGCTTTTTC TCTGTGAGG
56601 AAAGGGTGT GGGCTGGCC CGCCAGGGC TGGGTTAGG ATGAGCCAA
56651 GCTCAACCA AGCTCTCCCT TACCTGGTG GCAGCCCTG CTGGTAGTGG
56701 CATTCCTAT AAGAGAAGC CATGCCGCA GGACATCAC AGCTGTCCCT
56751 TGGCTTTGA TGGGTGGGG AGGAGGCCC TGGAGGGCAG CACTCTGCC
56801 TGCTGTCTG TCTGAGCCCT GTCTGGTTT CCTGAGAAC AGTCTCTGC
56851 AATGAGAGT GGTGTGAAT GTGCAGCTT CCAAGCCCT CAGAGGTAA
56901 TGGAGCAGC TCTCTGGTAC AGGCTGTCC AAGTTTCTAC AGTCTCTGA
56951 TCATTTCTC CAGAAAAGC CTGTGGAGT GAGCAGTGG AAGCATCCAT
57001 CTTAGGGTTC TGATGGTCT TTGGACCCC AGCCCTAGCT GGATCTGCT
57051 GTAGGGTAC CTGTACCCA GGGCTGGGT CTGGCCACTG AATGAGGCT
57101 ACGAGTGGG GTGGTGAAT AGAAGTACT GAGCCCTTC AGGTGAGAG
57151 AGTAAATGG GGTGGAAGC GGCCTTATG GGAGATGCT GTGAGAGG
57201 CTGCTCATC AGGGGAGGG CTCACAGCAT TCACATGTA CCAGCTCCT
57251 CACTGTATA AGGCAAGGT GTTTCTGCA ACCTGGTGT TGATGAAAG
57301 GGAGGCAAG GCAAGAAGC CATACTAAT GGCTGGGCT CAGAGAAAG
57351 TGGTATGTT CTCTGAGC TGACAGAGG GAGACGGAG GGAAGGTGT
57401 TTGCTCTTC CTGCCAAGG CCTTAGAGC AGAGAAGAG GATGCTTTG
57451 TCATAAGCA TCACAGGGA CTCTGAGGA CTGGGGAGG CTCTCTGTA
57501 CTTGGGAGG TCCCGATG GTAAATGAT GGATTTTCT CCCCACAGT
57551 GCGAAAACAG GAGATCATTA AGATTACAGA ACAGCTGATT GAAGCATCA
57601 ACAATGGGA CTTTGAAGC TACAGTAAG TAGAGACCA TTTTTTTTG
57651 TGACCTAAGT CATCTCCAA GGCCTTCCCT GCTTCCAGC AACATTAGG
57701 ACCCTGGGA AAGGGAGGT GGAAGTGGG CAAAGTATCT GAGTTAAGC
57751 CTCTCTTAA CTGGGAGCC TTCCAGGTAG ATTCCCTGAG CTCACCATG
57801 GTATCCCTGC AGTGGGCCA AAGCACAGG CTGAGTGGT CAGCAGGAG
57851 GCTGGAAGA TCTTTGCTG CTGTCTGGC ATGGCCACAG GTAGCTGCT
57901 GCTACTGGAT AGACACCGT GATAAGGAG GAAGACAAGT CACTCCATG

FIGURE 3S

57951 AAGCCIGATA GGCTGCTTTT TTTTTCCTCC CIGTAGGAAG ATTGIGATC
58001 CAGGOCITAC TTCCMTTGAG CCTGAGGCCC TTGGTAAOCT CGTGGAGGGG
58051 ATGGATTTC ATAGTTTATA CTTTGAGAAT CGTGAGTGGG TTGCTGCTGC
58101 TGATATACIC CTGCTTGCCC CTTTACCCCT TTGTCCTCTG CTCTGCTCA
58151 CCTTCTCATC CCAGTTGCCC ACTTTTCCCT TATTTGAOCT TGTGCTGCA
58201 CTCTACTCT GTATGCTTGT CCCCTTGTC CCCGATGGTT GTAGACAGGC
58251 ACCTTTGAAG GOCCTGCTCC TGAGCTCCAA GTGOCATICA TTCTGCAGCT
58301 GCTTTTGIGG AGTGGCAGTC ACCACAATCA AGCTCACTTA TTCTTGCCG
58351 GGGGGGGGG CTTAGCCTTG TAATCCCAAC ACTTTGGGAG GCTGAGGCTG
58401 GCGGATCAG AGGTGAGGAG ATCGAGGCA TCTGGCTTAA CAGGGTAAA
58451 CCCCCTCTCT ACTAAAAATA CAAAAAATA GCGGGGCTTG GTGGCAGTGC
58501 CTGTAGTCCC AGCTACTCGG GTGGCTGAGG CAGGAGAATG ATGTGAACCT
58551 GGGAGGACA GCTTGCACTG AGCCAAGATC AGGCCACIGC ACTCCAGCCT
58601 GGGCAACAGA GCAAGACTCC ATCTCAAAA AAAAGAAAA ATTATTAAAG
58651 CCTCACCTCT TTCCAAGAGG GATTGGAAGG AAACCCCTTG AGATTAGGTT
58701 GAGATGATCT CAGCACATAA GAACTAAGCT CTTGCTCTGC AGGTTTCACTA
58751 ATAGAGGAAA TTAAAAACAG GATAAGAATG TGCAAAACAG GGCACGTGTG
58801 GTGATTTGCG AGATCGGAAG TTGTGGCTAG AATCTTCTG ACTATGGAGG
58851 AAGGCAGACG TCTTGATATG GGGGTGGGGT GTACATTCIG GACAGTTGCT
58901 GAAAAATAAG GGGATAAGAA GCTGAATCAT CACCCCTCC CATCTTCTC
58951 TCTGCTCTAT GAGACCTCC CCTTCTCTAT TTTTATCTCT TCCCCTTTA
59001 TGTGCGGCT TCCCTATCCT GOCCTGAGTT ATAGTTAGTC ACTAACTCT
59051 CCGCTGGCTC CCACCCCTAT CACATCTCAG CTACATATAT AAATCTCTG
59101 TTATCTAAGT AATTCTATTA GCCAGAAGCA ATTCCAGAGT TTATATTAGT
59151 ACTAGGAAGG TGTATGTATG CCGCTGTCTA ACATTGGAAT TGAATAAAA
59201 TGTGATCTC AATAAAAGCA ACACAGTTT CACAGCATAT GCTGATAATG
59251 GCAATCCAAC TTTCTTTTGC TTTTCCCGAG AGAATCCIGG GAATATCCIG
59301 AGCTTGGTGC TTTGATGATT CTATTTCAGC TTGTGTGCT TAAAAAAAT
59351 TACAAATCAA TTTTGAATGG TTTAAGTTCA TGATTTTGT CTGCAGCCT
59401 AGCTAGGGGT GAGCCAAGCC TTATGAAATC TAAACTCAGC CTAACAGAAT
59451 AGAAATCTTA TAGGCTTTAG TTAAGAGTCA CATGTCTG AGTTCAGGTG
59501 TGTGATTTGA GCAATTAAT CCTTGAGCCT ATTTCTCAT CTATATAATG
59551 AGAAATATT ATCCACCAAG AAATACAGCT CCGGCATGTA AAACCCAGC
59601 ACAATGCTG ATTAAGAGG CAGCAGGTAC TGTACAGTGT ACCATCTTT
59651 CTGTCTCTT TGGATAAAGG AGACTAATGT AATGTGGCAT CCGGCTCT
59701 GAGGGGGGT CAGGGGTTC GGGGTGGGG GGGGGGTAC TTGGAGATT
59751 TGGGAGTGGT TGCTTGGAG ATGGTAAGAC TTGGAGTGC AGGCTGGAG
59801 GAAATGCGAG GTGCCAGGC CTGATGTCT CTTAOCCTAC CCACCTGCC
59851 CTGCAGTCT GTCCAAGAAC AGCAAGCCTA TCCATAACC CATCTTAAAC
59901 CCACAGTCC AGGTGATGG GAGGAGGCA GGTGCACTG CCTACATCCG
59951 CCTCACCCAG TACATGAGG GGCAGGGTGC GCTTGCACC AGCCAGTCCAG
60001 AAGAGACCCG GGTCTGGCAC CGTGGGATG GCAAGTGGCT CAATGTCCAC
60051 TATCAGTCT CAGGGGCCC TGCCGACCG CTGCAGTGC CTCAGCCACA
60101 GGTGCACCTG GTTACGGGG GAGAGGGGCT GGAAGGGCT GGGATAGGTG
60151 GGGTCAGAG AAGAAGAGAA GGCTGGGAG TGTCTCTGG AGAGGAGGTG
60201 TGGGCGTCC CAGAGGACTG GCAAAGCCTG GCAGAATGTT TGCAATAGT
60251 TATGCTTGG AATCAGACAG ACTAGGGTCT GGCTCGGTA CTCCAAATG
60301 GATGACCTCA GACAGGTAC TTCCCTCTCC TAAACTGTTT CCTTAGCTGT
60351 CAAGAAAGG CAGAGAGTGG TGCTACCTC ATTTAATCAT TGTGAGGATT
60401 AAGTAAGATA CTATAAGTAA AGCACTTAGT TAGTCTTAG CAATGGGAG
60451 GCAGTTTGT ATTTAAGCAT TAGCTTACC CACTTTCCC ACCTTCTCAG
60501 GCGACTTGG CCATGTGTT AGGTGCTTAA AGTCTCTGA ACTCATCTG
60551 GTGCTCATG TCTCTGTTC TGTACCACA TTCTGTCTG TTTGACAGGG
60601 GCTTTAGGAG ATTCCAGCC GAGGTCCAAC CTTCCAGCC AGTGGCTCTG
60651 GAGGGCTGA GTACAGCGG CAGTCCGTG TGTTTGAGT TTAACAAT
60701 TCAATTACAA AAGCGGAGC AGCCAATGCA CCGCCCTGCA TGCAAGCCCTC
60751 CCGCCCGCC TTCTGTCTG TCTCTGTGT ACCGAGGTG TTTTACATT
60801 TAGAAAAAA AAAAAAGAAA AAAAGATTGT TAAAAAAA AAGGAATCCA
60851 TACCATGATG CGTTTAAAA CCACGACAG CCGTTGGGT GCGAAGAAGG
60901 CAGGAGTATG TATGAGTCC ATCTTGGCAT GAGCAGTGGC TCACCCACCG
60951 GCTTGAAGA GGTGAGCTTG GCTCTCTG TCCCATGGA CTTAGGGGGA

FIGURE 3T

61001 CCAGGCAAGA ACTCTGACAG AGCTTTGGGG GCGTGATGT GATTGCAGCT
61051 CCTGAGGTTG CCTGCTTACC CCAGGCTTAG GAATGAACIT CTTTGGAACT
61101 TGCATAGGCG CCTAGAAATGG GGCTGATGAG AACATGGTGA CCATCAGACC
61151 TACTTGGGAG AGAAGCGAGA GCTCCAGCC TGCTGTGGAG GCAGCTGAGA
61201 AGTGGTGGCC TCAGGACTGA GAGCCCGGAC GTTGCCTGAC TGCTCTGTIT
61251 AGTGTAGAAG GGAAGAGAAT TGGTGTGCA GAAGTGTACC CGCATGAAG
61301 CCGATGAGAA ACCTCGTGT AGTCTGACAT GCACCTACTC ATCCATTCT
61351 ATAGGATGCA CAATGCGATGT GGGCCCTAAT ATTGAGGCTT TATCCCTGCA
61401 GCTAGGAGGG GGAGGGGTG TTGCTGCTTT GCTTGTGTTT TTCTTCTAAC
61451 CTGGCAAGGA GAGAGCCAGG CCTTGGTCAG GGCCTCCGTG CCGCTTTTGG
61501 CGGTCTGTTT TCTGTGCTGA TCTGGACCAT CTTTGTCTTG CCTTTTCACG
61551 GTAGTGGTCC CCATGCTGAC CCTCATCTGG GCTTGGGCC TCTGCCAAGT
61601 GCGCTGTGGG GATGGGAGGA GTGAGGCGT GGGAGAGAG GTGGTGGTGG
61651 TTTCTATGCA TTCAGGCTGC CTTTGGGGCT GCGTCCCTTC TTATCTTCC
61701 TTGCTGCACG TCCATCTCTT TTCTGTCTT TGAGATTGAC CTGACTGCTC
61751 TGGCAAGAG AAGAGGTGTC CTACAGAGG CCTCTTACT GACCACTGA
61801 AGTATAGACT TACTGCTGGA CAATCTGCAT GGGCATCACC CCTCCCGCA
61851 TGTAACCCAA AAGAGGTGTC CAGAGCCAG GCTTCTACCT TCATTGTCC
61901 TCTCTGTGCT CAAGGAGTTC CATTCAGGA GGAAGAGATC TATACCCIAA
61951 GCATATAGCA AAGAAGATAA TGGAGGAGCA ATTGGTCAATG GCGTTGGTIT
62001 CCTCAAAAC AACGCTGCAG ATTATCTGC ACAAACATCT CCACITTTGG
62051 GGGAAAGGTG GTAGATTCC AGTTCCTGG ACTACCTTCA GGAGSCAGGA
62101 GAGCTGGGAG AAGAGGCCAA GCTACAGGT TACTTGGGAG CCAGCTGAGA
62151 AGAGAGCAGA CTCACAGGTG CTGGTGTCTG GATTTAGCCA GGCCTCTCCG
62201 AGCACTCAT GCATGTGCCA GCGCTGGGC CCTAGCCCTT TCCGCGCTG
62251 CAGTCTGAG TGCCAGCAG CAAATCCCT CACCACAGG TTTGTGTTTG
62301 CTGGCTTGAA GACAAATGGT CTTAGAATTC ATTGAGACC ATAGCTTCAT
62351 ATGGCTGCTC CAGCCCACT TCTAGCATT CTACTCCCTC TCTGCGGCT
62401 AATGTCAGCA TCTATAGACA ATAGACTATT AAAAAATCAC CTTTAAACA
62451 AGAAACGGA GGCATTGTAT GCAGAAITTT TGCAAGCAA CATAGAAATA
62501 ATTTAAAAAT AGTGTGTGTT CTGAATGTG GTAGACCCCT CATAGCTTTG
62551 TTACAATGAA ACCITGAACT GAAATATTT AATAAAATTA CCTTTAAACA
62601 GTCCATTGTG TTACTGCTGT TGGAGGTTA CGGCCAGAG CGTAGATTTT
62651 AGCAGCCTGG GTTACCAGGT TGGAGAGAGT ACGTCCCTCT ACTCCCTTGG
62701 GGTACTTTTG AGAATAAAAC TTCTCATGC CTGTAATCC AGTACTTTGG
62751 GAGGCCAGG CGGCCGAATC ACGAGGTCAG GAGTTGAGA CCAGCCTGGC
62801 TAAT (SEQ ID NO:3)

FEATURES:

Exon: 1690-1694
Intron: 1695-2000
Exon: 2001-2095
Intron: 2096-14208
Exon: 14209-14268
Intron: 14269-21854
Exon: 21855-21909
Intron: 21910-22781
Exon: 22782-22847
Intron: 22848-25768
Exon: 25769-25841
Intron: 25842-25986
Exon: 25987-26089
Intron: 26090-26492
Exon: 26493-26576
Intron: 26577-27019
Exon: 27020-27114
Intron: 27115-27753
Exon: 27754-27876
Intron: 27877-32559

FIGURE 3U

Exon: 32560-32643
Intron: 32644-32889
Exon: 32890-32932
Intron: 32933-35499
Exon: 35500-35562
Intron: 35563-37589
Exon: 37590-37633
Intron: 37634-46979
Exon: 46980-47012
Intron: 47013-51017
Exon: 51018-51062
Intron: 51063-53371
Exon: 53372-53420
Intron: 53421-55458
Exon: 55459-55572
Intron: 55573-57549
Exon: 57550-57625
Intron: 57626-57986
Exon: 57987-58081
Intron: 58082-59856
Exon: 59857-60086

CHROMOSOME MAP POSITION:
Chromosome 10

ALLELIC VARIANTS (SNPs):

DNA

Position	Major	Minor	Domain
1603	G	A	Beyond ORF (5')
8632	T	-	Intron
19366	G	A	Intron
23770	T	C	Intron
31013	A	T G	Intron
33206	T	A	Intron
33263	G	A	Intron
33859	C	A	Intron
37254	T	C	Intron
40809	C	A	Intron
41025	T	C	Intron
42232	T	C	Intron
50477	G	A	Intron
55352	A	G	Intron
55914	A	G	Intron
56633	G	A	Intron

Context:

DNA

Position

1603 A C C C C C A C C C G G G G G G A G C C C G C A C T G C A G C C C C G C C C G C C C C C C C C A G A
C G T T T C C A G A G C T C A G A T G C G A G C T C C C G T T T G A C G G G A G G T C A A G G A A A T A G C A T G
G G A A G G G G A G T T C T T G A T G T C T G A C T G T G T C T C T C T T C C C T G C T G T C A G T T G A G C C G G
G A T G C A G T G A G A T G A A A C C G C T G T G G G G G G T T T G A G C C T C A C T T T G C C C A T G T T G A
G G A G A T T T C T C T T T C A G G G A T G A T A C C C T C T T T T A A T C T T T C C T T C C C G A C C T T C A
[G, A]
C T G T T C C T G C T G A G A G A G G G C A G G G T C T C T G C T C C C T T C T G C C C T G G T T C T C T T G G C
C G G A C C G C A G G G C T G T C T G A T G C A G C A G G T G T G T T T T C A G C A T G C C C A C C C G C T
C C T G A T G T G C A G C C T G A G G T G A G G C T G T T G C C T T G C C A G G G A C T G G A T G A G G G G T G G
G A G C G G G C A G C C A C C A C A T C T G T T C A G T G T C T G G G T G G C C G T C C T T T T G C C T C

FIGURE 3V

ATGTTGGATGGTGGTGGTACAGCGCGGTGGTGGTGCATGTACGTGAGTGGACTAGAG

8632 GA03GCGGCTCTGCTGCTTGGGAAGAATGAAGGCACTCAGGAGGCGAGCAAGTGG
GCGGCTTCCATGGAGGCTGAATCAGTGGGTTCAGGAAGTTCTCACAATCCATGTT
TAGGGTCATAGGCACAGACCTGCAAAATACCTTTGCAAGTTAAGANTGCTTTGAGAT
TGGAACTTGGGAGAGTCTCAGTACAGTACGAATGTGCATCCTTTCCACGTACAGAG
ATGTGATGTTTACGTGGCAGCAGGATCTTATTTGAAGCTAGTGCCTGGCATTGIGTTTTT
[T, -]
TTTTAGGAAATGTCACCTAAGTCAAGCAGGCGCATCCCTGAGAGGCGCATGGAGAATCTG
TGGCCAGGCTTCCCTGGGCGGCTGACCTGGCAGAGGAAGGAAAGGCGATTGGAGTAGGCT
TCTGTCTTCAGGCGCAGGGGGAGGTGGTTCAGGGCGAGGCTTGGTGCACCCCTTGGCTG
CAAGCTATCACCCTCCCTATCTGCTTCTCTTTCTGCTTCCCTGGTGCATCTGGTCACT
TCTGTGCGCCTTCCCTGTAATCGTGGCAGCCTTGGACCAAGTCTGAAGCACTTGGGCA

19366 CTCAGGAGGCTGAGACAGGAGATGGCTCAAGACCAAGGATCTCCAGCCAGCCTGGGCAAC
ATAGTGAGACCTGTCTCTTAAATAAAGAAATGAATCTGCTGTGCTAAATAG
GCACCTAGAGTGGCAGTCAATTTCTCTCTGTCTTCAGTGTCTGTAAATTTCTTTAC
AAATTAATAAATGTCTAGTACAGTCTTATTCAGATACAGCTTCTCCATCCCTCTGT
CTTGGCAGGTGCGCTTGTCTTGGGCAACATCAAGCTGTCTCTCTGCTGGGTGGCTA
[G, A]
AAGGATTAGTCTCTCTTGTCTGCTCTTCTCTTAATTCCTTCCCGCTTCTCCAC
CTGGGCTCTGTGTGTGGCTTCCCTGGGAGAGGCGAGAGCCAACTCACTCCATGTCTAGG
AGAGGCTTGGGTGCTGCTCTCTTGTGCTGTCTTGTGCTGTGGCGGGGCG
AGGGTGTGTGGGCGATGGGTGTGTGGGCGATGGGTGGGTCTGGCTGAGGCGAGG
CTCAGTCCAGGCGCAGGCGAGGCTGAGTGGCTCCACTTCTCTGAGATGGTGTGAGCAT

23770 CCCCCCTGCGCTTTTCTTCTTCTTGAATAATCTGGTGTGCTCAAGCCACTGTGCTGAG
GCTCTGGCATGATCCAGAGGTGCAAGACATGGTTTCTGTCTGAGGAGTGGAGAT
CTGGGCTGATAATCCAACTAGAGGCGGGAGCTTTAGGCTCTGTACCTTGTCTCT
AGACCACTAGACAGGCTTGGGTGGGCTCTCTCAACTTGAAGAGCTTCCCGGCA
CATGCTCAGGCTCTGCGCTCTGGAATCCCTGCTGCTCCCTCAACGCTCTCAGG
[T, C]
GCGTGTGAGCTGCTTCTCCCGCTTGGCTCTTCCCGAGCTTCTTCTGAGGCT
GATGCTCTACAACTGGTTTGTGATCTCTGCTGAGCTTATCTGGCTTATGTGGCAG
CTCTGGCTGCTCTTGGAGAGTGGGGAGTGCAGCTTCTCAGCAATTTCTCAACTTGA
AGGCCAATGTTTGTCTGATCAACTTCAGATGCTTCAGCTCGGGAAGAATTTCAAGTGG
GAGATGAATTCAGTGGCAGCAGGCGAGGAGCAGGCTCTGGGACGAGGAGGAGGAGT
GATG

31013 TCAGGAGGCGGTGGCTCACACCTGTAGTCCAGCACTTTGGGAGACAGGGTAGGTAGATC
ACTTGAAGCCCGAAGTTTGAAGCAGGCTGGGCAACATGGCAAAACCCATCTCTACAA
AAAAAAACTTTAAATAATAGCTGGTGTGTGTAAGCTGCTTACCTACTTGGGAGGCTGA
GATGAGAGGATCACTTGAAGCTAGAGAGGTGGAGTTGCAGTAAGCCATTATTTGTCTAC
TGCACTCCAGCTGGGCAACAGAGTGAGATGCTGTTTCAAAAAAATAAATTTTTTT
[A, T, G]
TTTAAGGAGAGGCTTAACTATAATCTATAGAGAAGATCTAGTCCAGAGGAAGAGTTGA
AGATCTCTGTCTAATTTAGGAAGCAAGGTTTGGACAGCAGAAAGAAGAGGGGCTCTG
AGCCAGGCGAGGGGTCCATCCCGGGATGACCATGATCCCTGAGACTTCTATAGT
GTGGAGGCGAGTGAAGATCGGCTTGTGAGTGAAGTCTGAGCTGAAAGGGGTTCTGTCTG
ATGACCTCTCATTTTGTCTTTTGGAGAATTTACACCGAGGAGGAGTAAATGAGAGCT

33206 CCATGCTGTCTCCAGCACTTCTCAGGTAATGTTTTCCAGCTGTGTACTTTGATTAATGC
CGAGGTGAGTGGATCAGGAATGGGCTGTGCAATCCCGGCAACGCTGGGTTTCTCTGGC
GTCTTGGGCGACACCTTGAACAGGCGAGTGGATCCCTGTTTGAAGGGCTGCTGCTGC
TGCTGAGTCTGCTCTCAGATTCAGGGGCTGGACTCACATTTGTGAATTTCTCTAG
AAGTTCCAGAGGAGTAGGCTGCCAAGTGTCTATGTAACCTTGTCTCTGATTTCTATT
[T, A]
AAGTCTCTGAAGACTCTCAGCACTTTACAGATTTTAGCCATTCTAGGATCTTGGAGGATG
TGCTGGGGAGAGAAAGAGAGATGAGGTACAGTGAAGTCTTCTCAATTTGCCAATTTGCCAC
CATTCATTTGCTGCTGGGAGATCTCTTACTTCAATTTGTGCAAGTGGAGATGACTAAT
AGAAATTTATCCAGATGTTTAAACCTTTTGTGGGAGTGTGCTTAAATAGTCCCTGAG
ATACCTAGCTATAAGAGTGAAGAAATAAGACAGCAGGAGAGAGGGAAGGAGTGTCT

FIGURE 3W

33263 TGCCGAGGTGAGTGGATCAGGAATGGGCTGTTGCCATCCCGGGCACCGCTGGGTTTCTCTC
GGCGTCTGGGCGCACACCTTGACCAGGGCGAGTGAGGATCCCTGTTTGGGGGCTGCTGC
TGCTGCTGAGTCCCTGCTGAGATTCAGGGGGCTGGACTCACATTTGTGAATGTGTTCC
TAGAATCTCCCAAGGAGTAGCCTGCCAACTTGCTATGTACCTTGTTCCTGGAATCTTT
ATTTAATCTCTCAGAGCTCTCAGACCTTTACAGATTTTAGCCATCTAGGATCTTGAG
[G, A]
ATGTGCTGGGGGAAGAAAAGAGAGATGAGGTACAGTGAGTCTTCTCAATTGCCAAATGTC
CACCATTCATTTGCCCTGCTGGACGATCTCTTACTTCATTTTGTCCAAGTGGAGATGACT
AATAGAAATTTATCCAGATGTTTAAACCTTTTGTGGCGACTTGTGCTTAAATAGTCCCT
GAGATACTAGCTATAACAGTGAAGAAATAAGACAGCAGGAGAGAGGGAAAGGAATGTG
CTTAAATTTGCATAAAGAATTGGGAGAGGTGGGAACAATAATTGTAAATCATACTTGAC

33859 TTGACATTTATTTTAAAGATGCAAGACCTCCACTCCCCCTCTTGCCCCACCCCTACCCCC
AACCCCTATTATTTGTTTGCCCTCAATTGGGAAGCACAGTGGCTTTTGTGAGGAAAAGA
TTAATGTGAGACTGAAGACAGAGAGGGCTCTGCCCCAGCTTGCCATCTCCCCGGTCTCTC
CTCCCTCTAACCCCTTGCCCTCAGTGTGTTGGTTCAAGACCCCCCTTCTCTTCCCATTA
ATAAGACTCCCTCCCTTGCTTCCCTCTGCACCAACATGGAAGGGGGTGTGTGGGAGC
[C, A]
TAAGCCACCCTCAGTGGGAGCCACTTCTGAATACCCGTCTGCTGGGCTGGCCCTGGGCT
GGCTCCAGGTAAAGCCAGGGCCCTTGCCCTGTGAGGATGCTGCAGGCAGGGAGCCTAGGGCT
TGCTGGTGTAGCTCAGAGCCATGGAGCTCCCGAAGGCCAGGGCTGGATAGTGAACCCGG
GGCTGGGGTGGCCCTGGCCTAGGGCTTCTCTTTGACCCCTGGTTTGGGGCTTGATCTTGT
GTATGGGTACCCACGAGGGGATACTGTGGTGTGGCTCCACCTCTCCAGATGGGAACA

37254 CATTATTCGCGAGTCTCTCTGCTCAGAGTCCAGAGTGGACACTGGGGAAAGGGT
GGCAGCTAGGACCCAGTGAACCTGGTGAGGACCTGCTCAGTGAAGGCTTCAACCCCTGG
CAAAACCCCTCCGTAGGGTGGTCTGGTTTCTGTGTCTGTGTCTGTGTCTGTGTCTGTGTCT
CTGTGTGAACCTGTGACACTCTGCTTCTTGAGAACACTCAGGAGATGTCTTGCACTCTGTC
AGTTTGGCCATCCAGAGAACTTCCATGGCACCTAGGGATGGAGCCCTCACTCTTTCACCC
[T, C]
GGCCTCTGCTTCCAGGCTGGGTGGAGCTGTCAAAGGCAGAGTCCCGAGTGGCCAGG
CGCTCCAGTACTGAGCATGGTTTCTCTCTAAGTGTGTGTCTCTCATGCCCCCTCTCCAC
GCAGAGGAGATCTCTGAGGTGCCACCCCTGAGGGCTCTGACGCCACTCAAGATCCCTCTCTT
GCTGAGAGGCTATAGGAGTGGCTCTTTTGGGGGTTTGGGGAGCCCTTGGCCCCCTGT
CAGACACAGCACTCTCTTGTGATCTGGCTGCCGACTTCAGGTGGGGAGAGGGTACAA

40809 GTGGCAAGGAAACAGAGGAAGGACAGAGAGGTAGGGGAAAAGAGAAATGTGCAGCAG
CTGCAGCTCTTCCAGGAACCTGAGGATGAGGGCTGGGCAGACATCATTAGGTAAAGG
CTTTAAATGAGGACGTGCGTGGGGAACCTAGCCCTGCAATGTGTGTGTGTGTGTGTGTGT
ATATGTGCTCAGTAAATGAGTTTATGCCACATCTCTTTGAGAAAAGAGCTTCAATATCA
TGGTGGGAACAGAGGCCAATGATCACCCAAAATTAAAGGCCAACCGGTATTCGAGC
[C, A]
GTGTGATGGGAGGGGTAAATATTTTATTTGAAAGAGTTTCTGTGACAAATAATCCCTCT
TAAACCCAGTGAAGCTGGCGTGGTGGCTCAGCCCTGTAATCCAGCACTTTGGGAGG
CCGAGGCGGGTGGATCAGGAGGTGAGGATCGAGACCATCTGGCTAACCGGTGAAC
CCCATCTCTACTGAAAATACAAAAAATTAGCCGGGTGTGGTGGCAGGCGCTGTAGTCC
AGCTACTTTGGGAGGTGAGGCGAGGAATGGCGTGAACCCGGAGGCGGAGCTTGAGTG

41025 TTGTGAGAAAAGAGCTTCAATATCATGGTGGGAACAGAGGCCAATGATCACCCAAAATTA
AAAGGCCAACCGGTATTCGAGCCGTTGTGATGGGAGGGTTAATATTTTATTTGAAAG
AGTTTCTGTGACAAATAATCCCTCTTAAACCCAGTGAAGCTGGGGTGGTGGCTCACG
CCCTGTAATCCAGCACTTTGGGAGGCGAGGCGGGTGGATCAGAGGTGAGGATCGAG
ACCATCTGGCTAACACGGTGAACCCCATCTCTACTGAAAATACAAAAAATTAGCCGGG
[T, C]
GTGGTGGCAGGCGCCCTGTAGTCCAGCTACTTGGGAGGTGAGGCGAGGAATGGCGTGA
AACCAGGAGGCGGAGCTTGCAGTGAAGCTGAGATTTGTGCACTGCACTCCATCTGGGTGA
CAGACCAAGACTCCGTCTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA
TAGGTGTGGTGGCTCATCTGTAAATCCAGCACTTTGGGATGCTGAGGTGGGCTGATCA
CTTGAGGCCAGGAGTTGAGACAGCCCTGGCCACATGGTGAACCCCTCTCTACTTAAA

FIGURE 3X

FIGURE 3Y